



#13

SEQUENCE LISTING

<110> AVENTIS PHARMA S.A.

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

<130> 446.001

<140> 09/786,880

<141> 2001-03-08

<150> EP98402255.8

<151> 1998-09-11

<160> 25

<170> PatentIn Ver. 2.1

<210> 1

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe

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cctgtcaaag ataatatattt gaaatttgat caaattaatc ataaatctcc tactttgatt 180
atgggtatat tgaatatgac tcctgattca tttagtgatg gtgggaaaca ttttgaaaa 240
gaactagata atattgtgaa gcaggcagag aaattagtca gtgagggtgc tacgattatt 300
gacattggag gagtttccac acgaccagga agtggtgaac ccactgagga agaagaattg 360
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<210> 2

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<212> DNA

<213> Candida albicans

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<221> CDS

<222> (1)..(2364)

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<221> gene

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Ile Thr Gly Lys Asp Ala Trp Asn Arg Pro Thr Pro Gln Pro Ile Thr	
20 25 30	
ata tca tta tct ttc aat act gat ttc cat aag gca tgc gaa ttg gat	144
Ile Ser Leu Ser Phe Asn Thr Asp Phe His Lys Ala Ser Glu Leu Asp	
35 40 45	
aat ttg aaa tac tca att aat tat gct gtt att acc aga aat gta act	192
Asn Leu Lys Tyr Ser Ile Asn Tyr Ala Val Ile Thr Arg Asn Val Thr	
50 55 60	
gaa ttt atg aaa tca aat gag cat tta aat ttc aag tca tta gga aat	240
Glu Phe Met Lys Ser Asn Glu His Leu Asn Phe Lys Ser Leu Gly Asn	
65 70 75 80	
att gct caa gca att agt gat att gga tta gat caa tct aga ggt ggt	288
Ile Ala Gln Ala Ile Ser Asp Ile Gly Leu Asp Gln Ser Arg Gly Gly	
85 90 95	
gga tct att gtg gat gtg acg ata aaa agt ttg aaa tca gaa ata aga	336
Gly Ser Ile Val Asp Val Thr Ile Lys Ser Leu Lys Ser Glu Ile Arg	
100 105 110	
gct gaa agt gtc gaa tat aaa att aat aga aac act ttg ggt caa ccc	384
Ala Glu Ser Val Glu Tyr Lys Ile Asn Arg Asn Thr Leu Gly Gln Pro	
115 120 125	
gtt cca tta gat att ttc caa gtt aat aaa ttg aga tta ttg acg att	432
Val Pro Leu Asp Ile Phe Gln Val Asn Lys Leu Arg Leu Leu Thr Ile	
130 135 140	
att gga gtt ttc aca ttt gaa aga tta caa aaa caa ata gtt gat gtt	480
Ile Gly Val Phe Thr Phe Glu Arg Leu Gln Lys Gln Ile Val Asp Val	
145 150 155 160	
gat ttg caa ttt aaa att gaa cct aat tcc aat tta tat ttc cat caa	528
Asp Leu Gln Phe Lys Ile Glu Pro Asn Ser Asn Leu Tyr Phe His Gln	
165 170 175	
ata att gct gat att gtt tca tac gtg gaa tca tct aat ttc aaa act	576
Ile Ile Ala Asp Ile Val Ser Tyr Val Glu Ser Ser Asn Phe Lys Thr	
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gta gaa gca ttg gtg tct aag att ggt caa ttg aca ttt cag aaa tat	624
Val Glu Ala Leu Val Ser Lys Ile Gly Gln Leu Thr Phe Gln Lys Tyr	
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gac gga gta gct gaa gtt gtt gct act gtc act aaa ccg aat gca ttt	672
Asp Gly Val Ala Glu Val Val Ala Thr Val Thr Lys Pro Asn Ala Phe	
210 215 220	

agt cat gtt gaa ggt gtc gga gta tca tct acc atg gtc aaa cca aat	720
Ser His Val Glu Gly Val Gly Val Ser Ser Thr Met Val Lys Asp Asn	
225 230 235 240	
ttc aaa gat atg gaa cca gtt aaa ttt gaa aac aca att gct caa act	768
Phe Lys Asp Met Glu Pro Val Lys Phe Glu Asn Thr Ile Ala Gln Thr	
245 250 255	
aat aga gca ttc aat tta cct gtt gaa aat gag aaa act gag gat tat	816
Asn Arg Ala Phe Asn Leu Pro Val Glu Asn Glu Lys Thr Glu Asp Tyr	
260 265 270	
acc ggg tac cac act gca ttt att gcc ttt gga tcc aat act gga aat	864
Thr Gly Tyr His Thr Ala Phe Ile Ala Phe Gly Ser Asn Thr Gly Asn	
275 280 285	
caa gta gaa aat att acc aat tca ttc gaa ttg ttg caa aaa tat gga	912
Gln Val Glu Asn Ile Thr Asn Ser Phe Glu Leu Leu Gln Lys Tyr Gly	
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atc acc ata gaa gca act tca tca ttg tac att tct aaa cca atg tat	960
Ile Thr Ile Glu Ala Thr Ser Ser Leu Tyr Ile Ser Lys Pro Met Tyr	
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tac ttg gat caa cca gat ttt ttc aat gga gta att aaa gtg aat ttc	1008
Tyr Leu Asp Gln Pro Asp Phe Phe Asn Gly Val Ile Lys Val Asn Phe	
325 330 335	
caa aac att tca cct ttc cag ttg ttg aaa att cta aaa gat att gaa	1056
Gln Asn Ile Ser Pro Phe Gln Leu Leu Lys Ile Leu Lys Asp Ile Glu	
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tat aaa cat tta gaa agg aaa aaa gac ttt gat aat ggg ccc aga tca	1104
Tyr Lys His Leu Glu Arg Lys Lys Asp Phe Asp Asn Gly Pro Arg Ser	
355 360 365	
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Ile Asp Leu Asp Ile Ile Leu Tyr Asp Asp Leu Gln Leu Asn Thr Glu	
370 375 380	
aat cta att att cca cat aaa tca atg tta gaa aga aca ttt gta tta	1200
Asn Leu Ile Ile Pro His Lys Ser Met Leu Glu Arg Thr Phe Val Leu	
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Gln Pro Leu Cys Glu Val Leu Pro Pro Asp Tyr Ile His Pro Ile Ser	
405 410 415	
gca gaa agt ttg cat agc cat tta caa caa tta ata aat gat aaa cct	1296
Ala Glu Ser Leu His Ser His Leu Gln Gln Leu Ile Asn Asp Lys Pro	
420 425 430	
caa gag aca gta caa gaa tcg tct gat tta tta caa ttt atc cca gtc	1344
Gln Glu Thr Val Gln Glu Ser Ser Asp Leu Leu Gln Phe Ile Pro Val	
435 440 445	
tct aga ttg cct gtc aaa gat aat att ttg aaa ttt gat caa att aat	1392

Ser	Arg	Leu	Pro	Val	Lys	Asp	Asn	Ile	Leu	Lys	Phe	Asp	Gln	Ile	Asn	
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cat	aaa	tct	cct	act	ttg	att	atg	ggg	ata	ttg	aat	atg	act	cct	gat	1440
His	Lys	Ser	Pro	Thr	Leu	Ile	Met	Gly	Ile	Leu	Asn	Met	Thr	Pro	Asp	
465					470					475					480	
tca	ttt	agt	gat	ggg	ggg	aaa	cat	ttt	gga	aaa	gaa	cta	gat	aat	act	1488
Ser	Phe	Ser	Asp	Gly	Gly	Lys	His	Phe	Gly	Lys	Glu	Leu	Asp	Asn	Thr	
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gtg	aag	cag	gca	gag	aaa	tta	gtc	agt	gag	ggg	gct	acg	att	att	gac	1536
Val	Lys	Gln	Ala	Glu	Lys	Leu	Val	Ser	Glu	Gly	Ala	Thr	Ile	Ile	Asp	
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Ile	Gly	Gly	Val	Ser	Thr	Arg	Pro	Gly	Ser	Val	Glu	Pro	Thr	Glu	Glu	
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gaa	gaa	ttg	gaa	cgt	gtg	att	cca	tta	att	aaa	gct	att	cgt	caa	tca	1632
Glu	Glu	Leu	Glu	Arg	Val	Ile	Pro	Leu	Ile	Lys	Ala	Ile	Arg	Gln	Ser	
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Leu	Asn	Pro	Asp	Leu	Leu	Lys	Val	Leu	Ile	Ser	Val	Asp	Thr	Tyr	Arg	
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agg	aac	gtt	gct	gaa	caa	agt	tta	ctt	gtg	ggg	gct	gac	ata	atc	aac	1728
Arg	Asn	Val	Ala	Glu	Gln	Ser	Leu	Leu	Val	Gly	Ala	Asp	Ile	Ile	Asn	
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gat	atc	tca	atg	ggc	aaa	tat	gat	gaa	aaa	ata	ttt	gat	gtg	gtt	gct	1776
Asp	Ile	Ser	Met	Gly	Lys	Tyr	Asp	Glu	Lys	Ile	Phe	Asp	Val	Val	Ala	
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aaa	tac	gga	tgt	cct	tat	atc	atg	aat	cat	act	cga	gga	tca	cct	aaa	1824
Lys	Tyr	Gly	Cys	Pro	Tyr	Ile	Met	Asn	His	Thr	Arg	Gly	Ser	Pro	Lys	
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acc	atg	tct	aaa	ttg	acc	aat	tat	gaa	tca	aat	aca	aat	gat	gat	att	1872
Thr	Met	Ser	Lys	Leu	Thr	Asn	Tyr	Glu	Ser	Asn	Thr	Asn	Asp	Asp	Ile	
	610					615					620					
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Ile	Glu	Tyr	Ile	Ile	Asp	Pro	Lys	Leu	Gly	His	Gln	Glu	Leu	Asp	Leu	
625					630					635					640	
tca	cct	gaa	atc	aag	aat	tta	ctc	aat	gga	atc	agt	cgt	gaa	ttg	agt	1968
Ser	Pro	Glu	Ile	Lys	Asn	Leu	Leu	Asn	Gly	Ile	Ser	Arg	Glu	Leu	Ser	
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tta	caa	atg	ttt	aaa	gcc	atg	gct	aaa	gga	gtg	aaa	aaa	tg	caa	att	2016
Leu	Gln	Met	Phe	Lys	Ala	Met	Ala	Lys	Gly	Val	Lys	Lys	Trp	Gln	Ile	
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Ile	Leu	Asp	Pro	Gly	Ile	Gly	Phe	Ala	Lys	Asn	Leu	Asn	Gln	Asn	Leu	

675

680

685

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aat gaa cgt gtt gat gat gtg aca atc aaa cat aaa tat tta agt ttt 2160
 Asn Glu Arg Val Asp Asp Val Thr Ile Lys His Lys Tyr Leu Ser Phe
 705 710 715 720

aat ggt gct tgt gtt ttg gtg ggg aca tca aga aag aag ttt ttg ggg 2208
 Asn Gly Ala Cys Val Leu Val Gly Thr Ser Arg Lys Lys Phe Leu Gly
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aca tta act ggt aat gaa gtg cct ctg gat cga gta ttt ggc act ggt 2256
 Thr Leu Thr Gly Asn Glu Val Pro Leu Asp Arg Val Phe Gly Thr Gly
 740 745 750

gca aca gtg tct gcg tgt att gaa caa aac act gat att gta aga gtt 2304
 Ala Thr Val Ser Ala Cys Ile Glu Gln Asn Thr Asp Ile Val Arg Val
 755 760 765

cat gat gtt aaa gaa atg aaa gat gta gta tgt ata agt gat gca att 2352
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 35 40 45

Asn Leu Lys Tyr Ser Ile Asn Tyr Ala Val Ile Thr Arg Asn Val Thr
 50 55 60

Glu Phe Met Lys Ser Asn Glu His Leu Asn Phe Lys Ser Leu Gly Asn
 65 70 75 80

Ile Ala Gln Ala Ile Ser Asp Ile Gly Leu Asp Gln Ser Arg Gly Gly
 85 90 95

Gly Ser Ile Val Asp Val Thr Ile Lys Ser Leu Lys Ser Glu Ile Arg
 100 105 110

Ala Glu Ser Val Glu Tyr Lys Ile Asn Arg Asn Thr Leu Gly Gln Pro
 115 120 125
 Val Pro Leu Asp Ile Phe Gln Val Asn Lys Leu Arg Leu Leu Thr Ile
 130 135 140
 Ile Gly Val Phe Thr Phe Glu Arg Leu Gln Lys Gln Ile Val Asp Val
 145 150 155 160
 Asp Leu Gln Phe Lys Ile Glu Pro Asn Ser Asn Leu Tyr Phe His Gln
 165 170 175
 Ile Ile Ala Asp Ile Val Ser Tyr Val Glu Ser Ser Asn Phe Lys Thr
 180 185 190
 Val Glu Ala Leu Val Ser Lys Ile Gly Gln Leu Thr Phe Gln Lys Tyr
 195 200 205
 Asp Gly Val Ala Glu Val Val Ala Thr Val Thr Lys Pro Asn Ala Phe
 210 215 220
 Ser His Val Glu Gly Val Gly Val Ser Ser Thr Met Val Lys Asp Asn
 225 230 235 240
 Phe Lys Asp Met Glu Pro Val Lys Phe Glu Asn Thr Ile Ala Gln Thr
 245 250 255
 Asn Arg Ala Phe Asn Leu Pro Val Glu Asn Glu Lys Thr Glu Asp Tyr
 260 265 270
 Thr Gly Tyr His Thr Ala Phe Ile Ala Phe Gly Ser Asn Thr Gly Asn
 275 280 285
 Gln Val Glu Asn Ile Thr Asn Ser Phe Glu Leu Leu Gln Lys Tyr Gly
 290 295 300
 Ile Thr Ile Glu Ala Thr Ser Ser Leu Tyr Ile Ser Lys Pro Met Tyr
 305 310 315 320
 Tyr Leu Asp Gln Pro Asp Phe Phe Asn Gly Val Ile Lys Val Asn Phe
 325 330 335
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 340 345 350
 Tyr Lys His Leu Glu Arg Lys Lys Asp Phe Asp Asn Gly Pro Arg Ser
 355 360 365
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 370 375 380
 Asn Leu Ile Ile Pro His Lys Ser Met Leu Glu Arg Thr Phe Val Leu
 385 390 395 400
 Gln Pro Leu Cys Glu Val Leu Pro Pro Asp Tyr Ile His Pro Ile Ser
 405 410 415

Ala Glu Ser Leu His Ser His Leu Gln Gln Leu Ile Asn Asp Lys Pro
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 Gln Glu Thr Val Gln Glu Ser Ser Asp Leu Leu Gln Phe Ile Pro Val
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 Ser Arg Leu Pro Val Lys Asp Asn Ile Leu Lys Phe Asp Gln Ile Asn
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 His Lys Ser Pro Thr Leu Ile Met Gly Ile Leu Asn Met Thr Pro Asp
 465 470 475 480
 Ser Phe Ser Asp Gly Gly Lys His Phe Gly Lys Glu Leu Asp Asn Thr
 485 490 495
 Val Lys Gln Ala Glu Lys Leu Val Ser Glu Gly Ala Thr Ile Ile Asp
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 Ile Gly Gly Val Ser Thr Arg Pro Gly Ser Val Glu Pro Thr Glu Glu
 515 520 525
 Glu Glu Leu Glu Arg Val Ile Pro Leu Ile Lys Ala Ile Arg Gln Ser
 530 535 540
 Leu Asn Pro Asp Leu Leu Lys Val Leu Ile Ser Val Asp Thr Tyr Arg
 545 550 555 560
 Arg Asn Val Ala Glu Gln Ser Leu Leu Val Gly Ala Asp Ile Ile Asn
 565 570 575
 Asp Ile Ser Met Gly Lys Tyr Asp Glu Lys Ile Phe Asp Val Val Ala
 580 585 590
 Lys Tyr Gly Cys Pro Tyr Ile Met Asn His Thr Arg Gly Ser Pro Lys
 595 600 605
 Thr Met Ser Lys Leu Thr Asn Tyr Glu Ser Asn Thr Asn Asp Asp Ile
 610 615 620
 Ile Glu Tyr Ile Ile Asp Pro Lys Leu Gly His Gln Glu Leu Asp Leu
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 Ser Pro Glu Ile Lys Asn Leu Leu Asn Gly Ile Ser Arg Glu Leu Ser
 645 650 655
 Leu Gln Met Phe Lys Ala Met Ala Lys Gly Val Lys Lys Trp Gln Ile
 660 665 670
 Ile Leu Asp Pro Gly Ile Gly Phe Ala Lys Asn Leu Asn Gln Asn Leu
 675 680 685
 Ala Val Ile Arg Asn Ala Ser Phe Phe Lys Lys Tyr Ser Ile Gln Ile
 690 695 700
 Asn Glu Arg Val Asp Asp Val Thr Ile Lys His Lys Tyr Leu Ser Phe
 705 710 715 720

Asn Gly Ala Cys Val Leu Val Gly Thr Ser Arg Lys Lys Phe Leu Gly
 725 730 735

Thr Leu Thr Gly Asn Glu Val Pro Leu Asp Arg Val Phe Gly Thr Gly
 740 745 750

Ala Thr Val Ser Ala Cys Ile Glu Gln Asn Thr Asp Ile Val Arg Val
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His Asp Val Lys Glu Met Lys Asp Val Val Cys Ile Ser Asp Ala Ile
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Tyr Lys Asn Val
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 <223> Description of Artificial Sequence: Probe

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 aatgtgggga attggaaacc aagttatcca actcatttat ttatatataa tgatttaatt 240
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 caacaaatca aatcaccgaa aaaagatgac gataagatgt attttatcaa tcttaaattcc 420
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Asn Arg Lys Ser Arg Ala Val Trp Gln Asn Asn Asn Thr Ser Thr His	
20 25 30	
aat aat cct tat gct aat tta agc act ggt gaa aaa agt agg agt cgc	144
Asn Asn Pro Tyr Ala Asn Leu Ser Thr Gly Glu Lys Ser Arg Ser Arg	
35 40 45	
cat aac act ggt agt tct tat gtt tct cca tat ggc ggc ggt aat gga	192
His Asn Thr Gly Ser Ser Tyr Val Ser Pro Tyr Gly Gly Gly Asn Gly	
50 55 60	
gag gag aat gct tat act ggg aat aac aac aaa tca aat act agt ggt	240
Glu Glu Asn Ala Tyr Thr Gly Asn Asn Asn Lys Ser Asn Thr Ser Gly	
65 70 75 80	
aat tta tta caa gtt cct gga gca gga gga gga gga gat ttg aat tct	288
Asn Leu Leu Gln Val Pro Gly Ala Gly Gly Gly Gly Asp Leu Asn Ser	
85 90 95	
aat aag aaa caa agt cga aga atg agt att cat gta tca gct cgt caa	336
Asn Lys Lys Gln Ser Arg Arg Met Ser Ile His Val Ser Ala Arg Gln	
100 105 110	
cat gga aga tca ttt tca caa act ggt cca att gat atg gca aat tta	384
His Gly Arg Ser Phe Ser Gln Thr Gly Pro Ile Asp Met Ala Asn Leu	
115 120 125	
ccg gca tta cct aaa ata ggt ggt gtt act act agt ggt gtt ggc ggt	432
Pro Ala Leu Pro Lys Ile Gly Gly Val Thr Thr Ser Gly Val Gly Gly	
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gct ggt ggt gat gtt atg aca agg act ggg gga ttg acg ata gaa caa	480
Ala Gly Gly Asp Val Met Thr Arg Thr Gly Gly Leu Thr Ile Glu Gln	
145 150 155 160	
aaa ata ttc aaa gaa tta agt caa gga tca gca gct gaa gtt gat gat	528
Lys Ile Phe Lys Glu Leu Ser Gln Gly Ser Ala Ala Glu Val Asp Asp	
165 170 175	
tat tac aag aca tta ttg aaa cag aaa aat tta atc act cgt gac att	576
Tyr Tyr Lys Thr Leu Leu Lys Gln Lys Asn Leu Ile Thr Arg Asp Ile	
180 185 190	
aag gat aat att aat cag aat caa aaa aat att tta caa tta aca aaa	624
Lys Asp Asn Ile Asn Gln Asn Gln Lys Asn Ile Leu Gln Leu Thr Lys	

195

200

205

gac ttg aaa gag acc caa gaa gaa ttg att gaa ttg aga gga acc act 672
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 210 215 220

aaa gaa tta tat gaa gtt tta ggt tat ttc aaa gaa tca gct caa cgt 720
 Lys Glu Leu Tyr Glu Val Leu Gly Tyr Phe Lys Glu Ser Ala Gln Arg
 225 230 235 240

aga tta gaa ttg gaa ttt gaa cca gaa aca caa aaa gaa ctt cat ctg 768
 Arg Leu Glu Leu Glu Phe Glu Pro Glu Thr Gln Lys Glu Leu His Leu
 245 250 255

cct caa aaa agt aat caa ttg ggt att cct agt aat aaa aag aaa gat 816
 Pro Gln Lys Ser Asn Gln Leu Gly Ile Pro Ser Asn Lys Lys Lys Asp
 260 265 270

cga tca tca att atg gtg ctt aaa aaa atg tgg gat tct caa tta caa 864
 Arg Ser Ser Ile Met Val Leu Lys Lys Met Trp Asp Ser Gln Leu Gln
 275 280 285

tca tta ttt aaa cat gtt gac ggt gca tca aaa ttt gtc caa cca tta 912
 Ser Leu Phe Lys His Val Asp Gly Ala Ser Lys Phe Val Gln Pro Leu
 290 295 300

ccc aat aga cac att gtc gcg gaa agt gga cga tgg ttt gaa gtt aat 960
 Pro Asn Arg His Ile Val Ala Glu Ser Gly Arg Trp Phe Glu Val Asn
 305 310 315 320

gtg ggg aat tgg aaa cca agt tat cca act cat tta ttt ata ttt aat 1008
 Val Gly Asn Trp Lys Pro Ser Tyr Pro Thr His Leu Phe Ile Phe Asn
 325 330 335

gat tta att tta att act gtt aaa aaa tca tca tct agt agt cag gaa 1056
 Asp Leu Ile Leu Ile Thr Val Lys Lys Ser Ser Ser Ser Ser Gln Glu
 340 345 350

cct act aca ggg gga agt aat ggt ggt tca aaa tcg aga tta caa gcg 1104
 Pro Thr Thr Gly Gly Ser Asn Gly Gly Ser Lys Ser Arg Leu Gln Ala
 355 360 365

gtt caa tgt tgg ccc tta act caa gta tca tta caa caa atc aaa tca 1152
 Val Gln Cys Trp Pro Leu Thr Gln Val Ser Leu Gln Gln Ile Lys Ser
 370 375 380

ccg aaa aaa gat gac gat aag atg tat ttt atc aat ctt aaa tcc aaa 1200
 Pro Lys Lys Asp Asp Asp Lys Met Tyr Phe Ile Asn Leu Lys Ser Lys
 385 390 395 400

tct tta agt tat gta tac ctg acg gat cgt tat gat cat ttt gtg aaa 1248
 Ser Leu Ser Tyr Val Tyr Leu Thr Asp Arg Tyr Asp His Phe Val Lys
 405 410 415

gtt acg gaa gca ttt aat aaa ggt aga aat gaa atg att caa agt gaa 1296
 Val Thr Glu Ala Phe Asn Lys Gly Arg Asn Glu Met Ile Gln Ser Glu
 420 425 430

aga tta tta gat tca aga ctt tca tct cct tca aat aat aat gga gat	1344
Arg Leu Leu Asp Ser Arg Leu Ser Ser Pro Ser Asn Asn Asn Gly Asp	
435 440 445	
tct aaa gaa gag aaa cga caa tta cgg gaa tca tta aga aac tca ggc	1392
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Asn Tyr Lys Glu Gly Val Thr Asp Asp Ala Gly Gly Ala Ala Thr Gly	
465 470 475 480	
ggt ggt agg aaa agt gcc ggt act cct aat aga aat agt act gat tac	1488
Gly Gly Arg Lys Ser Ala Gly Thr Pro Asn Arg Asn Ser Thr Asp Tyr	
485 490 495	
gtt tta cat gat ata tct gct cga gta cat tca cgt aat cga tca caa	1536
Val Leu His Asp Ile Ser Ala Arg Val His Ser Arg Asn Arg Ser Gln	
500 505 510	
gat tta ggg aat aat ttc aaa tta gct aat aat ggg aaa tca caa ttt	1584
Asp Leu Gly Asn Asn Phe Lys Leu Ala Asn Asn Gly Lys Ser Gln Phe	
515 520 525	
ttc aat gaa atc aaa act tta gaa gat cga tta gat gat gtt gac gtt	1632
Phe Asn Glu Ile Lys Thr Leu Glu Asp Arg Leu Asp Asp Val Asp Val	
530 535 540	
gaa ata tcg cat aat caa tat gct gaa gcc gtg gaa tta ata tca ata	1680
Glu Ile Ser His Asn Gln Tyr Ala Glu Ala Val Glu Leu Ile Ser Ile	
545 550 555 560	
att gaa tct aaa tta cgt aat att gaa aat gca tta act aat caa cgt	1728
Ile Glu Ser Lys Leu Arg Asn Ile Glu Asn Ala Leu Thr Asn Gln Arg	
565 570 575	
aat gga ggt aaa aat gtc aat att gct gat gaa tta tta ctt tta gat	1776
Asn Gly Gly Lys Asn Val Asn Ile Ala Asp Glu Leu Leu Leu Leu Asp	
580 585 590	
gta tca aaa ttg aaa att aaa aat cgg aaa gaa aat gta tct aat gga	1824
Val Ser Lys Leu Lys Ile Lys Asn Arg Lys Glu Asn Val Ser Asn Gly	
595 600 605	
tta ata ttt gat tta caa cat aat ata gct aaa ctt aaa caa gat gat	1872
Leu Ile Phe Asp Leu Gln His Asn Ile Ala Lys Leu Lys Gln Asp Asp	
610 615 620	
att gat aat att ttg acg tta ttt gat aat tta gag caa tta gat cga	1920
Ile Asp Asn Ile Leu Thr Leu Phe Asp Asn Leu Glu Gln Leu Asp Arg	
625 630 635 640	
ggg gtt caa gga tat ttg gat tca atg tca gct tat tta tca act aca	1968
Gly Val Gln Gly Tyr Leu Asp Ser Met Ser Ala Tyr Leu Ser Thr Thr	
645 650 655	

gta tca aaa tta att gtt gtt tta caa gga tca acg aaa atc gtt 2016
 Val Ser Lys Leu Ile Val Gly Leu Gln Gly Ser Thr Lys Ile Asp Val
 660 665 670

gtt aat tat ctt tcc aat tta atg gtt att aat gta tgc att gtg aaa 2064
 Val Asn Tyr Leu Ser Asn Leu Met Val Ile Asn Val Ser Ile Val Lys
 675 680 685

cgt aca att caa act tat gaa caa ata att gct cca att tta aaa cgt 2112
 Arg Thr Ile Gln Thr Tyr Glu Gln Ile Ile Ala Pro Ile Leu Lys Arg
 690 695 700

cat ggt gat gtt gat tca agt gga ttg att aat tgg tgt att gat gaa 2160
 His Gly Asp Val Asp Ser Ser Gly Leu Ile Asn Trp Cys Ile Asp Glu
 705 710 715 720

ttt act aaa ctt tgt aaa caa att aaa aaa cat ttg tat gga aca ttg 2208
 Phe Thr Lys Leu Cys Lys Gln Ile Lys Lys His Leu Tyr Gly Thr Leu
 725 730 735

ttg ata tct tct ggg att aat atg gaa act gat gaa cca att tat aaa 2256
 Leu Ile Ser Ser Gly Ile Asn Met Glu Thr Asp Glu Pro Ile Tyr Lys
 740 745 750

gtt aaa gaa aga aaa tta tat gat aat ttc ttg aag att atg caa cca 2304
 Val Lys Glu Arg Lys Leu Tyr Asp Asn Phe Leu Lys Ile Met Gln Pro
 755 760 765

caa ttg gaa gaa tta aaa ctg gtg gga tta aat gtt gat tat ata ttt 2352
 Gln Leu Glu Glu Leu Lys Leu Val Gly Leu Asn Val Asp Tyr Ile Phe
 770 775 780

gag tct ata tta aat ctt gaa 2373
 Glu Ser Ile Leu Asn Leu Glu
 785 790

<210> 6

<211> 791

<212> PRT

<213> Candida albicans

<400> 6

Met Asp Asn Leu Asp Pro Asn Ser Ser Leu Gln Val Glu Lys Leu Arg
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Asn Arg Lys Ser Arg Ala Val Trp Gln Asn Asn Asn Thr Ser Thr His
20 25 30

Asn Asn Pro Tyr Ala Asn Leu Ser Thr Gly Glu Lys Ser Arg Ser Arg
35 40 45

His Asn Thr Gly Ser Ser Tyr Val Ser Pro Tyr Gly Gly Gly Asn Gly
50 55 60

Glu Glu Asn Ala Tyr Thr Gly Asn Asn Asn Lys Ser Asn Thr Ser Gly
65 70 75 80

Asn Leu Leu Gln Val Pro Gly Ala Gly Gly Gly Gly Asp Leu Asn Ser
 85 90 95

Asn Lys Lys Gln Ser Arg Arg Met Ser Ile His Val Ser Ala Arg Gln
 100 105 110

His Gly Arg Ser Phe Ser Gln Thr Gly Pro Ile Asp Met Ala Asn Leu
 115 120 125

Pro Ala Leu Pro Lys Ile Gly Gly Val Thr Thr Ser Gly Val Gly Gly
 130 135 140

Ala Gly Gly Asp Val Met Thr Arg Thr Gly Gly Leu Thr Ile Glu Gln
 145 150 155 160

Lys Ile Phe Lys Glu Leu Ser Gln Gly Ser Ala Ala Glu Val Asp Asp
 165 170 175

Tyr Tyr Lys Thr Leu Leu Lys Gln Lys Asn Leu Ile Thr Arg Asp Ile
 180 185 190

Lys Asp Asn Ile Asn Gln Asn Gln Lys Asn Ile Leu Gln Leu Thr Lys
 195 200 205

Asp Leu Lys Glu Thr Gln Glu Glu Leu Ile Glu Leu Arg Gly Thr Thr
 210 215 220

Lys Glu Leu Tyr Glu Val Leu Gly Tyr Phe Lys Glu Ser Ala Gln Arg
 225 230 235 240

Arg Leu Glu Leu Glu Phe Glu Pro Glu Thr Gln Lys Glu Leu His Leu
 245 250 255

Pro Gln Lys Ser Asn Gln Leu Gly Ile Pro Ser Asn Lys Lys Lys Asp
 260 265 270

Arg Ser Ser Ile Met Val Leu Lys Lys Met Trp Asp Ser Gln Leu Gln
 275 280 285

Ser Leu Phe Lys His Val Asp Gly Ala Ser Lys Phe Val Gln Pro Leu
 290 295 300

Pro Asn Arg His Ile Val Ala Glu Ser Gly Arg Trp Phe Glu Val Asn
 305 310 315 320

Val Gly Asn Trp Lys Pro Ser Tyr Pro Thr His Leu Phe Ile Phe Asn
 325 330 335

Asp Leu Ile Leu Ile Thr Val Lys Lys Ser Ser Ser Ser Ser Gln Glu
 340 345 350

Pro Thr Thr Gly Gly Ser Asn Gly Gly Ser Lys Ser Arg Leu Gln Ala
 355 360 365

Val Gln Cys Trp Pro Leu Thr Gln Val Ser Leu Gln Gln Ile Lys Ser
 370 375 380

Pro Lys Lys Asp Asp Asp Lys Met Tyr Phe Ile Asn Leu Lys Ser Lys
 385 390 395 400
 Ser Leu Ser Tyr Val Tyr Leu Thr Asp Arg Tyr Asp His Phe Val Lys
 405 410 415
 Val Thr Glu Ala Phe Asn Lys Gly Arg Asn Glu Met Ile Gln Ser Glu
 420 425 430
 Arg Leu Leu Asp Ser Arg Leu Ser Ser Pro Ser Asn Asn Asn Gly Asp
 435 440 445
 Ser Lys Glu Glu Lys Arg Gln Leu Arg Glu Ser Leu Arg Asn Ser Gly
 450 455 460
 Asn Tyr Lys Glu Gly Val Thr Asp Asp Ala Gly Gly Ala Ala Thr Gly
 465 470 475 480
 Gly Gly Arg Lys Ser Ala Gly Thr Pro Asn Arg Asn Ser Thr Asp Tyr
 485 490 495
 Val Leu His Asp Ile Ser Ala Arg Val His Ser Arg Asn Arg Ser Gln
 500 505 510
 Asp Leu Gly Asn Asn Phe Lys Leu Ala Asn Asn Gly Lys Ser Gln Phe
 515 520 525
 Phe Asn Glu Ile Lys Thr Leu Glu Asp Arg Leu Asp Asp Val Asp Val
 530 535 540
 Glu Ile Ser His Asn Gln Tyr Ala Glu Ala Val Glu Leu Ile Ser Ile
 545 550 555 560
 Ile Glu Ser Lys Leu Arg Asn Ile Glu Asn Ala Leu Thr Asn Gln Arg
 565 570 575
 Asn Gly Gly Lys Asn Val Asn Ile Ala Asp Glu Leu Leu Leu Leu Asp
 580 585 590
 Val Ser Lys Leu Lys Ile Lys Asn Arg Lys Glu Asn Val Ser Asn Gly
 595 600 605
 Leu Ile Phe Asp Leu Gln His Asn Ile Ala Lys Leu Lys Gln Asp Asp
 610 615 620
 Ile Asp Asn Ile Leu Thr Leu Phe Asp Asn Leu Glu Gln Leu Asp Arg
 625 630 635 640
 Gly Val Gln Gly Tyr Leu Asp Ser Met Ser Ala Tyr Leu Ser Thr Thr
 645 650 655
 Val Ser Lys Leu Ile Val Gly Leu Gln Gly Ser Thr Lys Ile Asp Val
 660 665 670
 Val Asn Tyr Leu Ser Asn Leu Met Val Ile Asn Val Ser Ile Val Lys
 675 680 685

Arg Thr Ile Gln Thr Tyr Glu Gln Ile Ile Ala Pro Ile Leu Lys Arg
690 695 700

His Gly Asp Val Asp Ser Ser Gly Leu Ile Asn Trp Cys Ile Asp Glu
705 710 715 720

Phe Thr Lys Leu Cys Lys Gln Ile Lys Lys His Leu Tyr Gly Thr Leu
725 730 735

Leu Ile Ser Ser Gly Ile Asn Met Glu Thr Asp Glu Pro Ile Tyr Lys
740 745 750

Val Lys Glu Arg Lys Leu Tyr Asp Asn Phe Leu Lys Ile Met Gln Pro
755 760 765

Gln Leu Glu Glu Leu Lys Leu Val Gly Leu Asn Val Asp Tyr Ile Phe
770 775 780

Glu Ser Ile Leu Asn Leu Glu
785 790

<210> 7

<211> 343

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe

<400> 7

ctgcagtaaa ccctccagat ataacagact ctttatgtcc agtgatttcg ccaacaaatc 60
ttggtggttg ggtgtgtgtg gtccataagt atgccgtgtt gtcaccaccc ccagtcaata 120
ccattggcaa tttaggatgt gaaaaaatag taaatatact atcggtatgt ttatcaaaat 180
aagtccatga attgttgac atgtcaattt ctaaagtctc atgtcatca tctaattcca 240
tctctcatc ttcttcatcg ggtggcgctt gatcatcatc tgcaacttcc tcagccactt 300
cattaacatt gatatatctt tcttgagtat cgtctacgac gtc 343

<210> 8

<211> 1248

<212> DNA

<213> Candida albicans

<220>

<221> CDS

<222> (1)..(1245)

<220>

<221> gene

<222> (1)..(1245)

<223> gene CaIR012

<400> 8

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Met Ser His Gln Gln Glu Asp Val Val Asp Asp Thr Gln Glu Glu Tyr	
1 5 10 15	
atc aat gtt aat gaa gtg gct gag gaa gtt gca gat gat gat caa gcg	96
Ile Asn Val Asn Glu Val Ala Glu Glu Val Ala Asp Asp Asp Gln Ala	
20 25 30	
cca ccc gat gaa gaa gat gag gag atg gaa tta gat gat gag cat gag	144
Pro Pro Asp Glu Glu Asp Glu Glu Met Glu Leu Asp Asp Glu His Glu	
35 40 45	
act tta gaa att gac atg tcc aac aat tca tgg act tat ttt gat aaa	192
Thr Leu Glu Ile Asp Met Ser Asn Asn Ser Trp Thr Tyr Phe Asp Lys	
50 55 60	
cat acc gat agt ata ttt act att ttt tca cat cct aaa ttg cca atg	240
His Thr Asp Ser Ile Phe Thr Ile Phe Ser His Pro Lys Leu Pro Met	
65 70 75 80	
gta ttg act ggg ggt ggt gac aac acg gca tac tta tgg acc aca cac	288
Val Leu Thr Gly Gly Gly Asp Asn Thr Ala Tyr Leu Trp Thr Thr His	
85 90 95	
acc caa cca cca aga ttt gtt ggc gaa atc act gga cat aaa gag tct	336
Thr Gln Pro Pro Arg Phe Val Gly Glu Ile Thr Gly His Lys Glu Ser	
100 105 110	
gtt ata tct gga ggg ttt act gca gac ggc aag ttt gtt gtt act gca	384
Val Ile Ser Gly Gly Phe Thr Ala Asp Gly Lys Phe Val Val Thr Ala	
115 120 125	
gac atg aat gga tta att caa gtt ttc aaa gcc aca aaa gga ggt gaa	432
Asp Met Asn Gly Leu Ile Gln Val Phe Lys Ala Thr Lys Gly Gly Glu	
130 135 140	
cag tgg gtg aaa ttt ggt gaa ttg gac gaa gtt gaa gaa gtg ttg ttt	480
Gln Trp Val Lys Phe Gly Glu Leu Asp Glu Val Glu Glu Val Leu Phe	
145 150 155 160	
gtt act gtg cat cca aca tta cca ttc ttt gcc ttt ggt gct acc gat	528
Val Thr Val His Pro Thr Leu Pro Phe Phe Ala Phe Gly Ala Thr Asp	
165 170 175	
gga tct ata tgg gtc tac caa ata gac gaa tcc agt aaa ctg cta gtg	576
Gly Ser Ile Trp Val Tyr Gln Ile Asp Glu Ser Ser Lys Leu Leu Val	
180 185 190	
caa att atg tct ggg ttc tca cac aca tta gaa tgt aat ggt gct gta	624
Gln Ile Met Ser Gly Phe Ser His Thr Leu Glu Cys Asn Gly Ala Val	
195 200 205	
ttt ata caa gga aaa gat gaa aat gat ttg aca ttg gtc tct ata agt	672
Phe Ile Gln Gly Lys Asp Glu Asn Asp Leu Thr Leu Val Ser Ile Ser	

210	215	220	
gaa gat ggt act gtg gtg aac tgg aac tgt ttt aca gga caa gtg aat			720
Glu Asp Gly Thr Val Val Asn Trp Asn Cys Phe Thr Gly Gln Val Asn			
225	230	235	240
tat aaa ttg caa cct cat gat gac ttt aaa gga gtt gaa agt ccg tgg			768
Tyr Lys Leu Gln Pro His Asp Asp Phe Lys Gly Val Glu Ser Pro Trp			
	245	250	255
gtc acg gtc aaa gta cat ggt aat ctt gtg gcc att ggt ggc aga gat			816
Val Thr Val Lys Val His Gly Asn Leu Val Ala Ile Gly Gly Arg Asp			
	260	265	270
ggc cag cta tca att gtg aac aat gac act ggt aaa atc gtt cat act			864
Gly Gln Leu Ser Ile Val Asn Asn Asp Thr Gly Lys Ile Val His Thr			
	275	280	285
ctt aaa aca ttg gat aat gtc gac gac att gca gaa ctc tca att gag			912
Leu Lys Thr Leu Asp Asn Val Asp Asp Ile Ala Glu Leu Ser Ile Glu			
	290	295	300
gca ttg agt tgg tgt gaa agc aaa aat att aac ctc ttg gca gtg ggt			960
Ala Leu Ser Trp Cys Glu Ser Lys Asn Ile Asn Leu Leu Ala Val Gly			
305	310	315	320
ttg gtt tct ggt gac gtt tta tta ttt gat act cag caa tgg aga ttg			1008
Leu Val Ser Gly Asp Val Leu Leu Phe Asp Thr Gln Gln Trp Arg Leu			
	325	330	335
aga aag aac ttg aaa gtt gac gat gcc atc acc aaa tta caa ttt gtt			1056
Arg Lys Asn Leu Lys Val Asp Asp Ala Ile Thr Lys Leu Gln Phe Val			
	340	345	350
ggc gaa acc ccc att ttg gtg gga agt agt atg gat ggt aaa att tac			1104
Gly Glu Thr Pro Ile Leu Val Gly Ser Ser Met Asp Gly Lys Ile Tyr			
	355	360	365
aaa tgg gac gct aga act ggt gaa gag ttg ttt gct ggt gtg gga cac			1152
Lys Trp Asp Ala Arg Thr Gly Glu Glu Leu Phe Ala Gly Val Gly His			
	370	375	380
aac atg gga gta ttg gac ttt gct att tta gat gga ggt aaa aag ttg			1200
Asn Met Gly Val Leu Asp Phe Ala Ile Leu Asp Gly Gly Lys Lys Leu			
385	390	395	400
gtt act gct ggt gat gaa ggt gtt tca ttg gtc ttt gta cat gaa tag			1248
Val Thr Ala Gly Asp Glu Gly Val Ser Leu Val Phe Val His Glu			
	405	410	415

<210> 9

<211> 415

<212> PRT

<213> Candida albicans

<400> 9

Met	Ser	His	Gln	Gln	Glu	Asp	Val	Val	Asp	Asp	Thr	Gln	Glu	Leu	Tyr	1	5	10	15
Ile	Asn	Val	Asn	Glu	Val	Ala	Glu	Glu	Val	Ala	Asp	Asp	Asp	Gln	Ala	20	25	30	
Pro	Pro	Asp	Glu	Glu	Asp	Glu	Glu	Met	Glu	Leu	Asp	Asp	Glu	His	Glu	35	40	45	
Thr	Leu	Glu	Ile	Asp	Met	Ser	Asn	Asn	Ser	Trp	Thr	Tyr	Phe	Asp	Lys	50	55	60	
His	Thr	Asp	Ser	Ile	Phe	Thr	Ile	Phe	Ser	His	Pro	Lys	Leu	Pro	Met	65	70	75	80
Val	Leu	Thr	Gly	Gly	Gly	Asp	Asn	Thr	Ala	Tyr	Leu	Trp	Thr	Thr	His	85	90	95	
Thr	Gln	Pro	Pro	Arg	Phe	Val	Gly	Glu	Ile	Thr	Gly	His	Lys	Glu	Ser	100	105	110	
Val	Ile	Ser	Gly	Gly	Phe	Thr	Ala	Asp	Gly	Lys	Phe	Val	Val	Thr	Ala	115	120	125	
Asp	Met	Asn	Gly	Leu	Ile	Gln	Val	Phe	Lys	Ala	Thr	Lys	Gly	Gly	Glu	130	135	140	
Gln	Trp	Val	Lys	Phe	Gly	Glu	Leu	Asp	Glu	Val	Glu	Glu	Val	Leu	Phe	145	150	155	160
Val	Thr	Val	His	Pro	Thr	Leu	Pro	Phe	Phe	Ala	Phe	Gly	Ala	Thr	Asp	165	170	175	
Gly	Ser	Ile	Trp	Val	Tyr	Gln	Ile	Asp	Glu	Ser	Ser	Lys	Leu	Leu	Val	180	185	190	
Gln	Ile	Met	Ser	Gly	Phe	Ser	His	Thr	Leu	Glu	Cys	Asn	Gly	Ala	Val	195	200	205	
Phe	Ile	Gln	Gly	Lys	Asp	Glu	Asn	Asp	Leu	Thr	Leu	Val	Ser	Ile	Ser	210	215	220	
Glu	Asp	Gly	Thr	Val	Val	Asn	Trp	Asn	Cys	Phe	Thr	Gly	Gln	Val	Asn	225	230	235	240
Tyr	Lys	Leu	Gln	Pro	His	Asp	Asp	Phe	Lys	Gly	Val	Glu	Ser	Pro	Trp	245	250	255	
Val	Thr	Val	Lys	Val	His	Gly	Asn	Leu	Val	Ala	Ile	Gly	Gly	Arg	Asp	260	265	270	
Gly	Gln	Leu	Ser	Ile	Val	Asn	Asn	Asp	Thr	Gly	Lys	Ile	Val	His	Thr	275	280	285	
Leu	Lys	Thr	Leu	Asp	Asn	Val	Asp	Asp	Ile	Ala	Glu	Leu	Ser	Ile	Glu	290	295	300	

Ala Leu Ser Trp Cys Ser Lys Asn Ile Asn Leu Leu Ala Val Gly
 305 310 315 320
 Leu Val Ser Gly Asp Val Leu Leu Phe Asp Thr Gln Gln Trp Arg Leu
 325 330 335
 Arg Lys Asn Leu Lys Val Asp Asp Ala Ile Thr Lys Leu Gln Phe Val
 340 345 350
 Gly Glu Thr Pro Ile Leu Val Gly Ser Ser Met Asp Gly Lys Ile Tyr
 355 360 365
 Lys Trp Asp Ala Arg Thr Gly Glu Glu Leu Phe Ala Gly Val Gly His
 370 375 380
 Asn Met Gly Val Leu Asp Phe Ala Ile Leu Asp Gly Gly Lys Lys Leu
 385 390 395 400
 Val Thr Ala Gly Asp Glu Gly Val Ser Leu Val Phe Val His Glu
 405 410 415

<210> 10
 <211> 5544
 <212> DNA
 <213> Candida albicans

<220>
 <221> CDS
 <222> (1)..(5541)

<220>
 <221> gene
 <222> (1)..(5541)
 <223> gene CaJL039

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 aac acc ctc aag ttt gag tcc aat ata gat ttg gat aca atc gac ttc 96
 Asn Thr Leu Lys Phe Glu Ser Asn Ile Asp Leu Asp Thr Ile Asp Phe
 20 25 30
 acc agc atc aag aat gat ctt gca aat gtt ttg att aca cca gtc cct 144
 Thr Ser Ile Lys Asn Asp Leu Ala Asn Val Leu Ile Thr Pro Val Pro
 35 40 45
 ctg gat caa tca cgt agc aaa ctt gga gac gca tca aaa cca gtg gcg 192
 Leu Asp Gln Ser Arg Ser Lys Leu Gly Asp Ala Ser Lys Pro Val Ala
 50 55 60
 ttg ccc agt gga gat gag gtg aaa ttg aat caa gca tca att gaa att 240
 Leu Pro Ser Gly Asp Glu Val Lys Leu Asn Gln Ala Ser Ile Glu Ile
 65 70 75 80

act gga gtt tta tca aac gaa ttg gat tta gat gaa cta aat gca	288
Thr Gly Val Leu Ser Asn Glu Leu Asp Leu Asp Glu Leu Asn Thr Ala	
85 90 95	
gag ttg tta tat aac gca agt gac ttg agc tac aag aag gga acg tcc	336
Glu Leu Leu Tyr Asn Ala Ser Asp Leu Ser Tyr Lys Lys Gly Thr Ser	
100 105 110	
att ggc gat agt gct cga ttg gct tat tat tta aga gct cat tat ata	384
Ile Gly Asp Ser Ala Arg Leu Ala Tyr Tyr Leu Arg Ala His Tyr Ile	
115 120 125	
cta aac att gtt gga tac tta gtt tcg cat aaa cgt tta gat atc atc	432
Leu Asn Ile Val Gly Tyr Leu Val Ser His Lys Arg Leu Asp Ile Ile	
130 135 140	
act aac aac aac caa gtg ttg ttt gac aat att ttg aaa agt ttc agc	480
Thr Asn Asn Asn Gln Val Leu Phe Asp Asn Ile Leu Lys Ser Phe Ser	
145 150 155 160	
aag att tat act ttg agt ggt aaa tta aat gac atg att gac aag caa	528
Lys Ile Tyr Thr Leu Ser Gly Lys Leu Asn Asp Met Ile Asp Lys Gln	
165 170 175	
aaa gtt acc ggc gac atc aac aat ctt gca ttt atc aat tgt atc aat	576
Lys Val Thr Gly Asp Ile Asn Asn Leu Ala Phe Ile Asn Cys Ile Asn	
180 185 190	
tat tcc aga agt cag ttg ttt aat gca cac gag tta ttg gga caa gtt	624
Tyr Ser Arg Ser Gln Leu Phe Asn Ala His Glu Leu Leu Gly Gln Val	
195 200 205	
gta ttt gga tta gcg gat aat tat tat gag agt tat ggc aca cta aac	672
Val Phe Gly Leu Ala Asp Asn Tyr Tyr Glu Ser Tyr Gly Thr Leu Asn	
210 215 220	
aac tat aat tcc tta gtg gag ttt ata ctg aaa aat atc agc gat gaa	720
Asn Tyr Asn Ser Leu Val Glu Phe Ile Leu Lys Asn Ile Ser Asp Glu	
225 230 235 240	
gat gtt ttt gtt atc cat ttt tta cca tcc act tta caa ttg ttc aag	768
Asp Val Phe Val Ile His Phe Leu Pro Ser Thr Leu Gln Leu Phe Lys	
245 250 255	
aaa tta ctt caa cta ggt gag gaa tct tta gtc gat cag ttt tac aag	816
Lys Leu Leu Gln Leu Gly Glu Glu Ser Leu Val Asp Gln Phe Tyr Lys	
260 265 270	
act ata acc tct tcc ata cta aaa gat tat gaa gcc aac aat ttt tcc	864
Thr Ile Thr Ser Ser Ile Leu Lys Asp Tyr Glu Ala Asn Asn Phe Ser	
275 280 285	
aaa agt gaa gat att gac ttg tca aaa tca aaa ttg tct ggc ttt gaa	912
Lys Ser Glu Asp Ile Asp Leu Ser Lys Ser Lys Leu Ser Gly Phe Glu	
290 295 300	
ata gtc aca agc ttt att ttt cta act gag ttt att cca tgg tgc aag	960

Ile Val Thr Ser Phe	Ile Phe Leu Thr Glu Phe Ile Pro Trp	Lys	
305	310 315	320	
cag ctg tca agt aga acc gcg aaa tac gat ttc aaa gat gat ata tta		1008	
Gln Leu Ser Ser Arg Thr Ala Lys Tyr Asp Phe Lys Asp Asp Ile Leu	325 330 335		
aag tat atg gaa ttc ttg ata agt tat gga gtt atg gaa cga tta tta		1056	
Lys Tyr Met Glu Phe Leu Ile Ser Tyr Gly Val Met Glu Arg Leu Leu	340 345 350		
tca tac tgt tct gaa acc agc aat gca aaa act cag caa gtg tac gac		1104	
Ser Tyr Cys Ser Glu Thr Ser Asn Ala Lys Thr Gln Gln Val Tyr Asp	355 360 365		
tgg tca aac atg tac gat ttc aga gca ttg ctt caa aag aat ttc cca		1152	
Trp Ser Asn Met Tyr Asp Phe Arg Ala Leu Leu Gln Lys Asn Phe Pro	370 375 380		
cga ctt aca cca gca aaa ttt cat tat cct ggc aat caa gaa ttg ttg		1200	
Arg Leu Thr Pro Ala Lys Phe His Tyr Pro Gly Asn Gln Glu Leu Leu	385 390 395 400		
aat gca gtt aga ccg gga tat gaa aat ata tcc aaa ttg att gac att		1248	
Asn Ala Val Arg Pro Gly Tyr Glu Asn Ile Ser Lys Leu Ile Asp Ile	405 410 415		
tcc ttt ttg acg tta gat cca tcg ctt aat gag acg ttg gtt tca cct		1296	
Ser Phe Leu Thr Leu Asp Pro Ser Leu Asn Glu Thr Leu Val Ser Pro	420 425 430		
ttt ttc cag agc ttt ttc agt gtg ttt ata tct aat gcc gca gtt gtt		1344	
Phe Phe Gln Ser Phe Phe Ser Val Phe Ile Ser Asn Ala Ala Val Val	435 440 445		
atg acc tct tta agg gac tca gag gaa gat ttt gtt tta tcg tcg ttg		1392	
Met Thr Ser Leu Arg Asp Ser Glu Glu Asp Phe Val Leu Ser Ser Leu	450 455 460		
aat gaa agt gac gaa gag gaa gaa gaa gaa gaa agc gac agc gac gaa		1440	
Asn Glu Ser Asp Glu Glu Glu Glu Glu Glu Glu Ser Asp Ser Asp Glu	465 470 475 480		
gat tct tcg acc cca aaa aac aaa gaa aaa tca gct ggg tta gac ctt		1488	
Asp Ser Ser Thr Pro Lys Asn Lys Glu Lys Ser Ala Gly Leu Asp Leu	485 490 495		
gac aag att gcc cag cgt gct gaa tta gaa agg ttc tac ttg gct ttc		1536	
Asp Lys Ile Ala Gln Arg Ala Glu Leu Glu Arg Phe Tyr Leu Ala Phe	500 505 510		
gcg tac acc tac aac aat cga cct gaa ttg tgt gcg tta ttt tgg ggg		1584	
Ala Tyr Thr Tyr Asn Asn Arg Pro Glu Leu Cys Ala Leu Phe Trp Gly	515 520 525		
aac gag cag gta act cat gac att ata gga ttt att tcc tgg gga ctt		1632	
Asn Glu Gln Val Thr His Asp Ile Ile Gly Phe Ile Ser Trp Gly Leu			

530

535

540

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ggg tcg ttg gca tct gct ggt gca gag gca act tca agg ata tgg gag 1728
 Gly Ser Leu Ala Ser Ala Gly Ala Glu Ala Thr Ser Arg Ile Trp Glu
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 Ile Leu Val His Asn Asn Asn Asn Ala Ser Thr Arg Lys Asn Asp Phe
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tca aag gta tcc gtt gac tcc ctt tat gat tcg ttg aaa tat tac att 1824
 Ser Lys Val Ser Val Asp Ser Leu Tyr Asp Ser Leu Lys Tyr Tyr Ile
 595 600 605

gac tct tta aat gaa agc ttt gaa caa gat tta aat gcc caa ttg atg 1872
 Asp Ser Leu Asn Glu Ser Phe Glu Gln Asp Leu Asn Ala Gln Leu Met
 610 615 620

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 625 630 635 640

cag gac ctt gat gat tct ggc gag aat aga att gtt ata gag ttg gcc 1968
 Gln Asp Leu Asp Asp Ser Gly Glu Asn Arg Ile Val Ile Glu Leu Ala
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gag gat tca ctt gtc ctc att tca ggg ttt att caa tta ctt tct gca 2016
 Glu Asp Ser Leu Val Leu Ile Ser Gly Phe Ile Gln Leu Leu Ser Ala
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att gtg aag aat ttg aac act aag aat gaa aga agc aaa gaa atc aaa 2064
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 675 680 685

tcc gtg gta tac act aga ttc tca cca atc att aaa ggg ttt tta aaa 2112
 Ser Val Val Tyr Thr Arg Phe Ser Pro Ile Ile Lys Gly Phe Leu Lys
 690 695 700

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 Phe Asp Asn Leu Ile Asn Gly Ser Arg Phe Leu Gln Val Asp Ala Ser
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 Ile Gln Ser Thr Asn Asn Pro Lys Phe Ile Asp Leu Pro Asn Val Phe
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gtc agt gat gac tcg aga att ata ttg acg aac ctc att cta acc ttt 2256
 Val Ser Asp Asp Ser Arg Ile Ile Leu Thr Asn Leu Ile Leu Thr Phe
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 Leu Gly Asp Phe Val Thr Asn Asp Ser Asp Pro Tyr Ile Arg Tyr Glu
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Pro Glu Asp Lys Lys Asp Asp Ala Phe Arg His Ile Lys Arg Lys Tyr	
785 790 795 800	
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Asn Ser Lys Lys Asn Val Pro Ile Asn Gln Ala Phe Ser Thr Asn Leu	
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Thr His Leu Ser Gln Ile Gly Asn Phe Thr Val Leu Val Lys Lys Leu	
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Gly Ile Trp Pro Tyr Ile Glu Phe Leu Met Gln Asn Val Phe Ala Asn	
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Pro Arg Thr Ile Phe Asp Cys Ile Tyr Tyr Pro Lys Asn Leu Gly Thr	
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His Gly Val Ala Asp Phe Tyr Glu Val Ile Leu Phe His Leu Ser Ala	
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Lys Ala Ile Ser Ile Leu Lys Gly Val Ser Gln Ser Lys Phe Phe Val	
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Thr Arg Val Ser Ser Ala Asp Pro Leu Leu Asn Asn Asp Arg Leu	
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Ile Thr Thr Phe Glu Asn Ile Asp Glu Ser Ile Lys Ile Lys Phe Ala	
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Glu Ile Leu Asp Phe Val Leu Gly Asn Leu Asn Gln Phe Asp Gly Lys	
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Val Ala Thr Thr Ala His Phe Leu Leu Gly Tyr Lys Val Lys Gly Asp	
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Tyr Asn Asn Gly Asn Asn His Ile Ile Asp Val Gly Pro Ala Lys Leu	
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Ser Ser Leu Ile Leu Gln Ile Leu Ile Lys Leu Cys Gln Asp Pro Ile	
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1780 1785 1790

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Lys Ser Val Asn Arg Leu Val Val Gly Val Met Lys Arg Asp Phe Leu
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Thr Ser Ile Lys Asn Asp Leu Ala Asn Val Leu Ile Thr Pro Val Pro
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Leu Asp Gln Ser Arg Ser Lys Leu Gly Asp Ala Ser Lys Pro Val Ala
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Leu Pro Ser Gly Asp Glu Val Lys Leu Asn Gln Ala Ser Ile Glu Ile
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Thr Gly Val Leu Ser Asn Glu Leu Asp Leu Asp Glu Leu Asn Thr Ala
85 90 95

Glu Leu Leu Tyr Asn Ala Ser Asp Leu Ser Tyr Lys Lys Gly Thr Ser
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Ile Gly Asp Ser Ala Arg Leu Ala Tyr Tyr Leu Arg Ala His Tyr Ile
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Lys Ile Tyr Thr Leu Ser Gly Lys Leu Asn Asp Met Ile Asp Lys Gln
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Lys Val Thr Gly Asp Ile Asn Asn Leu Ala Phe Ile Asn Cys Ile Asn
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Tyr Ser Arg Ser Gln Leu Phe Asn Ala His Glu Leu Leu Gly Gln Val
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Val Phe Gly Leu Ala Asp Asn Tyr Tyr Glu Ser Tyr Gly Thr Leu Asn
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Asn Tyr Asn Ser Leu Val Glu Phe Ile Leu Lys Asn Ile Ser Asp Glu
225 230 235 240

Asp Val Phe Val Ile His Phe Leu Pro Ser Thr Leu Gln Leu Phe Lys
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Lys Leu Leu Gln Leu Gly Glu Glu Ser Leu Val Asp Gln Phe Tyr Lys
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Ile Val Thr Ser Phe Ile Phe Leu Thr Glu Phe Ile Pro Trp Cys Lys
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Gln Leu Ser Ser Arg Thr Ala Lys Tyr Asp Phe Lys Asp Asp Ile Leu
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 Trp Ser Asn Met Tyr Asp Phe Arg Ala Leu Leu Gln Lys Asn Phe Pro
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 Arg Leu Thr Pro Ala Lys Phe His Tyr Pro Gly Asn Gln Glu Leu Leu
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 Ser Gly Thr Ile Ala Asn Lys Arg Asp Arg Val Asn Leu Gln Leu Asn
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Phe Val Lys Leu His His Ser Val Ala Val Ile Asn Tyr Leu Phe Glu
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Cys Gly Asn Gln Phe Asp Gly Asp Leu Gln Ile Asp Ala Ser Asn Val	1285	1290	1295	
Phe Val Asp Asn Gln Ala Ser Thr Gln Ala Phe Phe Ser Phe Ile Asn	1300	1305	1310	
Gln Arg Asn Leu Ile Leu Gln Tyr Leu Ser Leu Glu Phe His Ser Val	1315	1320	1325	-
Lys Ser Arg Thr Lys Arg Glu Tyr Tyr Ser Lys Val Leu Thr Asn Asp	1330	1335	1340	
Lys Glu Phe Val Asn Arg Thr Pro Lys Val Leu Thr Phe Leu Asn Ile	1345	1350	1355	1360
Leu Asn Tyr Ser Phe Lys Asn Phe Glu Val Gln Lys Tyr Glu Trp Leu	1365	1370	1375	
Asp Gln Lys Phe Asn Val Ser Leu Leu Leu Ala Glu Val Asn Ala Gln	1380	1385	1390	
Lys Asn Gly Thr Leu Asp Phe Ser Val Leu Thr Lys Val Phe Arg Leu	1395	1400	1405	
Leu Cys Gln Thr Ser Asn Leu Ile Thr Pro Glu Ser Lys Gln Leu Phe	1410	1415	1420	
Ala Glu Glu Ile Met Val Glu Gly Ser Lys Ile Ser Asp Phe Val Thr	1425	1430	1435	1440
Lys Tyr Leu Val Ser Thr Asp Leu Lys Asp Val Gln Leu Lys Cys Leu	1445	1450	1455	
His Ser Trp Cys Gln Leu Ile Glu Ile Leu Val Thr Asp Ser Gly Ile	1460	1465	1470	
Asn Ser Leu Asn Phe Ile Leu Glu Val Leu Gln Val Ile Ile Pro Lys	1475	1480	1485	
Ile Asn Asp Tyr Phe Asp Val Asp Ile Leu Phe Ser Glu Glu Met Val	1490	1495	1500	
Ser Leu Cys Val Leu Leu Phe Asp Leu Tyr Asp Gln Leu Thr Leu Ala	1505	1510	1515	1520
Asp Arg Lys Gly Glu Asp Phe Ala Leu Gly Ile Glu Arg Leu Ile Pro	1525	1530	1535	
Leu Phe Gln Thr Cys Ile Ala Gly Ile Leu Asn Ser Asn Ser Thr Pro	1540	1545	1550	

Ser Leu Arg Ser Asp Leu Tyr Val Val Gly Asn Lys Phe Leu Leu Lys
 1555 1560 1565

Cys Phe Glu Arg Glu Ser Phe Leu Lys Gln Val Met His Ile Ile Lys
 1570 1575 1580

Ser Val Asp Lys Lys Phe Phe Gln Val Ile Cys Asn Asp Ala Ile Tyr
 1585 1590 1595 1600

Ser Glu Gly Pro Ser Arg Ile Thr Ser Thr Leu Phe Leu Glu Ser Leu
 1605 1610 1615

Val His Leu Gly Thr Leu Val Lys Val Asp Phe Ile Leu Asn Ala Leu
 1620 1625 1630

Ile Lys Asn Asn Ala Leu Leu Leu Leu Val Arg Ser Val Lys Arg Thr
 1635 1640 1645

Asp Ala Met Ile Lys Leu Cys Gln Glu Lys Asn Ser Gly Val Thr Leu
 1650 1655 1660

Asp His Phe Ile Phe Asp Leu Met Ala Phe Lys Ala Thr Leu Tyr Phe
 1665 1670 1675 1680

Phe Val Arg Val Ala Lys Ser Lys Asn Gly Ala Leu Gln Leu Ile Gln
 1685 1690 1695

Asn Glu Leu Phe Ser Ile Leu His Gln Ser Lys Phe Leu Gln Ile Asp
 1700 1705 1710

Pro Asp Ile Gly Leu Ser Leu Arg Ile Glu Glu Val Gln Asp His Lys
 1715 1720 1725

Thr Val Asn Val Asn Val Leu Leu Asp Thr Pro Leu Ser Ile Thr Asp
 1730 1735 1740

Leu Val Asp Pro Tyr Lys Leu Arg Ser Glu Asn Thr Ile Ser Tyr Phe
 1745 1750 1755 1760

Glu Phe Leu Val Pro Ile Phe Gln Leu Leu Thr Thr Val Leu Leu Ser
 1765 1770 1775

Met Gly Pro Asn Tyr Gln Pro Ala Ile Ile Gln Thr Arg Glu Leu Met
 1780 1785 1790

Lys Ser Val Asn Arg Leu Val Val Gly Val Met Lys Arg Asp Phe Leu
 1795 1800 1805

Val Glu Thr Lys Gln Ile Gly Gln Gly Leu Tyr Lys Glu Glu Ser His
 1810 1815 1820

Glu Leu Val Ser Leu Lys Glu Leu Val Lys Leu Phe Ile Leu Ile Asp
 1825 1830 1835 1840

Ser Leu Ala His Tyr Ser Val
 1845

<210> 12
<211> 575
<212> DNA
<213> Artificial Sequence

<220>
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Fragment to Sc YJL039c

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<223> Any AA

<220>
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<220>
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<222> (407)..(408)
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<220>
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taattgcagg ttgataattt ggtcccattg acaataacac tgttgtaagt agctgaaata 120
ttggtacaag gaactcaaaa tatgatatag tgttttcact tcgcaacttg tatggatcca 180

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ccaagtcagt tatcgaaagt ggagtatcta gcaaaacatt tacattgaca gtcttgtgat 240
cttgaacttc ttcaattcgt aaacttaaac caatatctgg atcaatctgc aaaaacttcg 300
actgatgcaa aattgaaaac aattcatttt ggaatcannn nnanaantna aaaaaaatat 360
atatntnttt tttttttttt ttntttnttt tttattttat cttacannac accccaacac 420
aacaccaaac cnaaaaacac ccaacacctc catcttgtcc cgcttttctc tcacattttt 480
tctctactac tatcacacaa tctataaaac atacaccccc tcaacccctc ctccccaaca 540
aacctacctc cctcaactcc tatttctctcc cttec 575

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<210> 13
<211> 921
<212> DNA
<213> Candida albicans

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<220>
<221> CDS
<222> (1)..(918)

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<220>
<221> gene
<222> (1)..(918)
<223> gene CaOR110

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<400> 13
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Met Thr Ile Glu Thr Ile Tyr Ile Ala Arg His Gly Tyr Arg Ser Asn
  1             5             10             15

tgg tta cca cca cca cac cca cca aat cct act ggt att gac agt gac 96
Trp Leu Pro Pro Pro His Pro Pro Asn Pro Thr Gly Ile Asp Ser Asp
          20             25             30

ccg gct tta gca cca cat ggt gtt gaa caa gcc caa cag tta gct gcc 144
Pro Ala Leu Ala Pro His Gly Val Glu Gln Ala Gln Gln Leu Ala Ala
      35             40             45

tat ctt aca tca tta cct aca cat gaa aag cct gaa ttt att att gct 192
Tyr Leu Thr Ser Leu Pro Thr His Glu Lys Pro Glu Phe Ile Ile Ala
      50             55             60

tca cct ttt tat cgt tgt ata gaa acg tcg aga ccc att gcc gaa atg 240
Ser Pro Phe Tyr Arg Cys Ile Glu Thr Ser Arg Pro Ile Ala Glu Met
      65             70             75             80

ttg gac ttg aag att gct tta gaa aga gga gtt ggt gaa tgg ttt cgt 288
Leu Asp Leu Lys Ile Ala Leu Glu Arg Gly Val Gly Glu Trp Phe Arg
          85             90             95

aaa aat aga gat acc aaa cca gtt ccc ggt gat tac aca caa ttg aga 336
Lys Asn Arg Asp Thr Lys Pro Val Pro Gly Asp Tyr Thr Gln Leu Arg

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100	105	110	
aca ttt ttc gat aaa tta ttg atc gat gaa gat act tgg cca aga gat Thr Phe Phe Asp Lys Leu Leu Ile Asp Glu Asp Thr Trp Pro Arg Asp 115 120 125			384
aac tta aat gtt ata cct aat att gaa gga gaa gat tat gat gaa atc Asn Leu Asn Val Ile Pro Asn Ile Glu Gly Glu Asp Tyr Asp Glu Ile 130 135 140			432
tac gat cgt gcc aaa ttg ttt tgg aaa aag ttt att cct gaa ttt gaa Tyr Asp Arg Ala Lys Leu Phe Trp Lys Lys Phe Ile Pro Glu Phe Glu 145 150 155 160			480
aag aaa ttc ccc gaa att aaa aat gtg ttg ata gtt aca cat gca gca Lys Lys Phe Pro Glu Ile Lys Asn Val Leu Ile Val Thr His Ala Ala 165 170 175			528
acg aaa att gct tta gga tca gct tta tta cag tta aaa tca gtt act Thr Lys Ile Ala Leu Gly Ser Ala Leu Leu Gln Leu Lys Ser Val Thr 180 185 190			576
gat gtt ata gat gat aat caa act gtg tta cgt gct ggt gca tgt tca Asp Val Ile Asp Asp Asn Gln Thr Val Leu Arg Ala Gly Ala Cys Ser 195 200 205			624
tta tcc aaa ttt gtt aga gat ggc gaa gat aaa acc aat cat act att Leu Ser Lys Phe Val Arg Asp Gly Glu Asp Lys Thr Asn His Thr Ile 210 215 220			672
caa tgg aaa att gtc atg aat ggt aat tgt gaa ttc ttg aca cag ggt Gln Trp Lys Ile Val Met Asn Gly Asn Cys Glu Phe Leu Thr Gln Gly 225 230 235 240			720
gaa gaa atg aac tgg gat ttc cgt cgt ggt gtt gaa gcc ggg tca gct Glu Glu Met Asn Trp Asp Phe Arg Arg Gly Val Glu Ala Gly Ser Ala 245 250 255			768
gaa gat ata gcg caa aga aag gca gca gca gaa gca gaa gca aaa gca Glu Asp Ile Ala Gln Arg Lys Ala Ala Ala Glu Ala Glu Ala Lys Ala 260 265 270			816
ttg aag aaa aat gaa caa acc aaa tcc gat ggt ccc atc act gaa tct Leu Lys Lys Asn Glu Gln Thr Lys Ser Asp Gly Pro Ile Thr Glu Ser 275 280 285			864
gcc act ggg gca gaa ata gat ggg aat gaa gat gaa ttt gaa gta cgt Ala Thr Gly Ala Glu Ile Asp Gly Asn Glu Asp Glu Phe Glu Val Arg 290 295 300			912
aaa act tga Lys Thr 305			921

<210> 14

<211> 306

<212> PRT

<213> Candida albicans

<400> 14

Met	Thr	Ile	Glu	Thr	Ile	Tyr	Ile	Ala	Arg	His	Gly	Tyr	Arg	Ser	Asn
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Trp	Leu	Pro	Pro	Pro	His	Pro	Pro	Asn	Pro	Thr	Gly	Ile	Asp	Ser	Asp
			20					25					30		
Pro	Ala	Leu	Ala	Pro	His	Gly	Val	Glu	Gln	Ala	Gln	Gln	Leu	Ala	Ala
		35					40					45			
Tyr	Leu	Thr	Ser	Leu	Pro	Thr	His	Glu	Lys	Pro	Glu	Phe	Ile	Ile	Ala
	50					55					60				
Ser	Pro	Phe	Tyr	Arg	Cys	Ile	Glu	Thr	Ser	Arg	Pro	Ile	Ala	Glu	Met
65					70				75						80
Leu	Asp	Leu	Lys	Ile	Ala	Leu	Glu	Arg	Gly	Val	Gly	Glu	Trp	Phe	Arg
			85						90					95	
Lys	Asn	Arg	Asp	Thr	Lys	Pro	Val	Pro	Gly	Asp	Tyr	Thr	Gln	Leu	Arg
			100					105					110		
Thr	Phe	Phe	Asp	Lys	Leu	Leu	Ile	Asp	Glu	Asp	Thr	Trp	Pro	Arg	Asp
		115					120					125			
Asn	Leu	Asn	Val	Ile	Pro	Asn	Ile	Glu	Gly	Glu	Asp	Tyr	Asp	Glu	Ile
	130					135					140				
Tyr	Asp	Arg	Ala	Lys	Leu	Phe	Trp	Lys	Lys	Phe	Ile	Pro	Glu	Phe	Glu
145					150					155					160
Lys	Lys	Phe	Pro	Glu	Ile	Lys	Asn	Val	Leu	Ile	Val	Thr	His	Ala	Ala
			165						170					175	
Thr	Lys	Ile	Ala	Leu	Gly	Ser	Ala	Leu	Leu	Gln	Leu	Lys	Ser	Val	Thr
			180					185					190		
Asp	Val	Ile	Asp	Asp	Asn	Gln	Thr	Val	Leu	Arg	Ala	Gly	Ala	Cys	Ser
	195						200					205			
Leu	Ser	Lys	Phe	Val	Arg	Asp	Gly	Glu	Asp	Lys	Thr	Asn	His	Thr	Ile
	210					215					220				
Gln	Trp	Lys	Ile	Val	Met	Asn	Gly	Asn	Cys	Glu	Phe	Leu	Thr	Gln	Gly
225					230					235					240
Glu	Glu	Met	Asn	Trp	Asp	Phe	Arg	Arg	Gly	Val	Glu	Ala	Gly	Ser	Ala
			245						250					255	
Glu	Asp	Ile	Ala	Gln	Arg	Lys	Ala	Ala	Ala	Glu	Ala	Glu	Ala	Lys	Ala
			260				265						270		
Leu	Lys	Lys	Asn	Glu	Gln	Thr	Lys	Ser	Asp	Gly	Pro	Ile	Thr	Glu	Ser
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Ala Thr Gly Ala Glu Ile Asp Gly Asn Glu Asp Glu Phe Glu Val Arg
 290 295 300

Lys Thr
 305

<210> 15
 <211> 1454
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Splice Variant -

<220>
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 <222> (1)..(1452)
 <223> gene CaOR110 Splice Variant

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 Met Thr Ile Glu Thr Ile Tyr Ile Ala Arg His Gly Tyr Arg Ser Asn
 1 5 10 15

tgg tta cca cca cca cac cca cca aat cct act ggt att gac agt gac 96
 Trp Leu Pro Pro Pro His Pro Pro Asn Pro Thr Gly Ile Asp Ser Asp
 20 25 30

ccg gct tta gca cca cat ggt gtt gaa caa gcc caa cag tta gct gcc 144
 Pro Ala Leu Ala Pro His Gly Val Glu Gln Ala Gln Gln Leu Ala Ala
 35 40 45

tat ctt aca tca tta cct aca cat gaa aag cct gaa ttt att att gct 192
 Tyr Leu Thr Ser Leu Pro Thr His Glu Lys Pro Glu Phe Ile Ile Ala
 50 55 60

tca cct ttt tat cgt tgt ata gaa acg tcg aga ccc att gcc gaa atg 240
 Ser Pro Phe Tyr Arg Cys Ile Glu Thr Ser Arg Pro Ile Ala Glu Met
 65 70 75 80

ttg gac ttg aag att gct tta gaa aga gga gtt ggt gaa tgg ttt cgt 288
 Leu Asp Leu Lys Ile Ala Leu Glu Arg Gly Val Gly Glu Trp Phe Arg
 85 90 95

aaa aat aga gat acc aaa cca gtt ccc ggt gat tac aca caa ttg aga 336
 Lys Asn Arg Asp Thr Lys Pro Val Pro Gly Asp Tyr Thr Gln Leu Arg
 100 105 110

aca ttt ttc gat aaa tta ttg atc gat gaa gat act tgg cca aga gat 384
 Thr Phe Phe Asp Lys Leu Leu Ile Asp Glu Asp Thr Trp Pro Arg Asp
 115 120 125

aac tta aat gtt ata cct aat att gaa gga gaa gat tat gat gaa atc 432
 Asn Leu Asn Val Ile Pro Asn Ile Glu Gly Glu Asp Tyr Asp Glu Ile
 130 135 140

tac gat cgt gcc aaa ttg ttt tgg aaa aag ttt att cct gaa ttt gaa	480
Tyr Asp Arg Ala Lys Leu Phe Trp Lys Lys Phe Ile Pro Glu Phe Glu	
145 150 155 160	
aag aaa ttc ccc gaa att aaa aat gtg ttg ata gtt aca cat gca gca	528
Lys Lys Phe Pro Glu Ile Lys Asn Val Leu Ile Val Thr His Ala Ala	
165 170 175	
acg aaa att gct tta gga tca gct tta tta cag tta aaa tca gtt act	576
Thr Lys Ile Ala Leu Gly Ser Ala Leu Leu Gln Leu Lys Ser Val Thr	
180 185 190	
gat gtt ata gat gat aat caa act gtg tta cgt gct ggt gca tgt tca	624
Asp Val Ile Asp Asp Asn Gln Thr Val Leu Arg Ala Gly Ala Cys Ser	
195 200 205	
tta tcc aaa ttt gtt aga gat ggc gaa gat aaa acc aat cat act att	672
Leu Ser Lys Phe Val Arg Asp Gly Glu Asp Lys Thr Asn His Thr Ile	
210 215 220	
caa tgg aaa att gtc atg aat ggt aat tgt gaa ttc ttg aca cag ggt	720
Gln Trp Lys Ile Val Met Asn Gly Asn Cys Glu Phe Leu Thr Gln Gly	
225 230 235 240	
gaa gaa atg aac tgg gat ttc cgt cgt ggt gtt gaa gcc ggg tca gct	768
Glu Glu Met Asn Trp Asp Phe Arg Arg Gly Val Glu Ala Gly Ser Ala	
245 250 255	
gaa gat ata gcg caa aga aag gca gca gca gaa gca gaa gca aaa gca	816
Glu Asp Ile Ala Gln Arg Lys Ala Ala Ala Glu Ala Glu Ala Lys Ala	
260 265 270	
ttg aag aaa aat gaa caa acc aaa tcc gat ggt ccc atc act gaa tct	864
Leu Lys Lys Asn Glu Gln Thr Lys Ser Asp Gly Pro Ile Thr Glu Ser	
275 280 285	
gcc act ggg gca gaa ata gat ggg aat gaa gat gaa ttt gaa aca ttt	912
Ala Thr Gly Ala Glu Ile Asp Gly Asn Glu Asp Glu Phe Glu Thr Phe	
290 295 300	
tat gta acc atc gat ata cct tca att tcg aat aaa atc gac aat gaa	960
Tyr Val Thr Ile Asp Ile Pro Ser Ile Ser Asn Lys Ile Asp Asn Glu	
305 310 315 320	
gaa gaa cca cca tca agg aca ggt caa gct cca aaa ttc aaa aac aat	1008
Glu Glu Pro Pro Ser Arg Thr Gly Gln Ala Pro Lys Phe Lys Asn Asn	
325 330 335	
att atc aag cct tca gca caa ctc caa ttt act gat tta aaa gaa gat	1056
Ile Ile Lys Pro Ser Ala Gln Leu Gln Phe Thr Asp Leu Lys Glu Asp	
340 345 350	
cat cca tta gta aaa ata tcg aac aat act ata tct gct caa ggc tcg	1104
His Pro Leu Val Lys Ile Ser Asn Asn Thr Ile Ser Ala Gln Gly Ser	
355 360 365	

tcg	tcg	tcg	tcg	tta	tta	gcg	tcg	aaa	aat	gga	ttt	aat	agt	cat	act	1152
Ser	Ser	Ser	Ser	Leu	Ser	Ala	Ser	Lys	Asn	Gly	Phe	Asn	Ser	His	Thr	
370				375				380								

cac	aat	tca	gga	gtc	att	gat	cca	tca	gca	ctt	ata	gat	ggg	aaa	att	1200
His	Asn	Ser	Gly	Val	Ile	Asp	Pro	Ser	Ala	Leu	Ile	Asp	Gly	Lys	Ile	
385		390				395				400						

tat	cag	act	gat	tgg	aat	caa	tta	caa	ggt	act	gaa	cta	ata	ttt	gat	1248
Tyr	Gln	Thr	Asp	Trp	Asn	Gln	Leu	Gln	Gly	Thr	Glu	Leu	Ile	Phe	Asp	
405				410				415								

gaa	aat	ggt	caa	ttt	ata	ggc	aag	gtt	aag	gaa	cat	ttg	act	tgc	aat	1296
Glu	Asn	Gly	Gln	Phe	Ile	Gly	Lys	Val	Lys	Glu	His	Leu	Thr	Cys	Asn	
420			425				430									

aat	aac	aca	aaa	ttc	aca	tta	aaa	aag	gca	gaa	gaa	gta	gaa	caa	ctt	1344
Asn	Asn	Thr	Lys	Phe	Thr	Leu	Lys	Lys	Ala	Glu	Glu	Val	Glu	Gln	Leu	
435			440				445									

cgt	tca	gca	gat	gat	tct	atc	atg	gat	ata	gat	caa	gac	tca	caa	gga	1392
Arg	Ser	Ala	Asp	Asp	Ser	Ile	Met	Asp	Ile	Asp	Gln	Asp	Ser	Gln	Gly	
450		455				460										

caa	caa	cca	gct	aga	agt	cag	ttc	tta	aaa	aga	gca	att	gtg	gct	gct	1440
Gln	Gln	Pro	Ala	Arg	Ser	Gln	Phe	Leu	Lys	Arg	Ala	Ile	Val	Ala	Ala	
465		470				475				480						

aga	gcc	aaa	ggt	aa												1454
Arg	Ala	Lys	Gly													

<210> 16
 <211> 484
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Splice Variant

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		20						25					30		
Pro	Ala	Leu	Ala	Pro	His	Gly	Val	Glu	Gln	Ala	Gln	Gln	Leu	Ala	Ala
		35					40					45			
Tyr	Leu	Thr	Ser	Leu	Pro	Thr	His	Glu	Lys	Pro	Glu	Phe	Ile	Ile	Ala
	50					55					60				
Ser	Pro	Phe	Tyr	Arg	Cys	Ile	Glu	Thr	Ser	Arg	Pro	Ile	Ala	Glu	Met
65					70					75					80
Leu	Asp	Leu	Lys	Ile	Ala	Leu	Glu	Arg	Gly	Val	Gly	Glu	Trp	Phe	Arg

Lys Asn Arg Asp Thr Lys Pro Val Pro Gly Asp Tyr Thr Gln Leu Arg
 100 105 110
 Thr Phe Phe Asp Lys Leu Leu Ile Asp Glu Asp Thr Trp Pro Arg Asp
 115 120 125
 Asn Leu Asn Val Ile Pro Asn Ile Glu Gly Glu Asp Tyr Asp Glu Ile
 130 135 140
 Tyr Asp Arg Ala Lys Leu Phe Trp Lys Lys Phe Ile Pro Glu Phe Glu
 145 150 155 160
 Lys Lys Phe Pro Glu Ile Lys Asn Val Leu Ile Val Thr His Ala Ala
 165 170 175
 Thr Lys Ile Ala Leu Gly Ser Ala Leu Leu Gln Leu Lys Ser Val Thr
 180 185 190
 Asp Val Ile Asp Asp Asn Gln Thr Val Leu Arg Ala Gly Ala Cys Ser
 195 200 205
 Leu Ser Lys Phe Val Arg Asp Gly Glu Asp Lys Thr Asn His Thr Ile
 210 215 220
 Gln Trp Lys Ile Val Met Asn Gly Asn Cys Glu Phe Leu Thr Gln Gly
 225 230 235 240
 Glu Glu Met Asn Trp Asp Phe Arg Arg Gly Val Glu Ala Gly Ser Ala
 245 250 255
 Glu Asp Ile Ala Gln Arg Lys Ala Ala Ala Glu Ala Glu Ala Lys Ala
 260 265 270
 Leu Lys Lys Asn Glu Gln Thr Lys Ser Asp Gly Pro Ile Thr Glu Ser
 275 280 285
 Ala Thr Gly Ala Glu Ile Asp Gly Asn Glu Asp Glu Phe Glu Thr Phe
 290 295 300
 Tyr Val Thr Ile Asp Ile Pro Ser Ile Ser Asn Lys Ile Asp Asn Glu
 305 310 315 320
 Glu Glu Pro Pro Ser Arg Thr Gly Gln Ala Pro Lys Phe Lys Asn Asn
 325 330 335
 Ile Ile Lys Pro Ser Ala Gln Leu Gln Phe Thr Asp Leu Lys Glu Asp
 340 345 350
 His Pro Leu Val Lys Ile Ser Asn Asn Thr Ile Ser Ala Gln Gly Ser
 355 360 365
 Ser Ser Ser Ser Leu Ser Ala Ser Lys Asn Gly Phe Asn Ser His Thr
 370 375 380
 His Asn Ser Gly Val Ile Asp Pro Ser Ala Leu Ile Asp Gly Lys Ile

385

390

395

400

Tyr Gln Thr Asp Trp Asn Gln Leu Gln Gly Thr Glu Leu Ile Phe Asp
 405 410 415

Glu Asn Gly Gln Phe Ile Gly Lys Val Lys Glu His Leu Thr Cys Asn
 420 425 430

Asn Asn Thr Lys Phe Thr Leu Lys Lys Ala Glu Glu Val Glu Gln Leu
 435 440 445

Arg Ser Ala Asp Asp Ser Ile Met Asp Ile Asp Gln Asp Ser Gln Gly
 450 455 460

Gln Gln Pro Ala Arg Ser Gln Phe Leu Lys Arg Ala Ile Val Ala Ala
 465 470 475 480

Arg Ala Lys Gly

<210> 17

<211> 2877

<212> DNA

<213> Candida albicans

<220>

<221> CDS

<222> (1)..(2874)

<220>

<221> gene

<222> (1)..(2874)

<223> gene CaMR212

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cct gct ggg aaa gca gtg gac aaa aaa ccc aac tcg tcc gag tta agt 96
 Pro Ala Gly Lys Ala Val Asp Lys Lys Pro Asn Ser Ser Glu Leu Ser
 20 25 30

tat tta tta tac tat gca tcc act cgt aga gtc aaa tta gaa aag gtg 144
 Tyr Leu Leu Tyr Tyr Ala Ser Thr Arg Arg Val Lys Leu Glu Lys Val
 35 40 45

att aat ttt ttg aaa gat aaa act cat cat gat gtt ggt aga aac cgt 192
 Ile Asn Phe Leu Lys Asp Lys Thr His His Asp Val Gly Arg Asn Arg
 50 55 60

act ggt aat tta caa gtc aca tta gcc att att cag gaa tta atc aaa 240
 Thr Gly Asn Leu Gln Val Thr Leu Ala Ile Ile Gln Glu Leu Ile Lys
 65 70 75 80

aaa tgt agt gaa aac ttg aat gtt ttt gcc ttt caa gtg tgc tat atc 288
 Lys Cys Ser Glu Asn Leu Asn Val Phe Ala Phe Gln Val Cys Tyr Ile

85

90

95

ttg caa ctg att gcc aac act aag gat ctt gcc ttg tgt aaa aat gtt	336
Leu Gln Leu Ile Ala Asn Thr Lys Asp Leu Ala Leu Cys Lys Asn Val	
100 105 110	
gtc aaa aca ttt ggt gtt ttg tgt gaa aac ttg gat ggt ggg ttg ttc	384
Val Lys Thr Phe Gly Val Leu Cys Glu Asn Leu Asp Gly Gly Leu Phe	
115 120 125	
aca ggt gat aag gag ttt ata aag att ttc act gaa gtt ttc caa aca	432
Thr Gly Asp Lys Glu Phe Ile Lys Ile Phe Thr Glu Val Phe Gln Thr	
130 135 140	
tta gtt tcc ttt ggt aag gac aga tcg ggt gtt act cag tat gat tgg	480
Leu Val Ser Phe Gly Lys Asp Arg Ser Gly Val Thr Gln Tyr Asp Trp	
145 150 155 160	
cag atg att tct tta atg gct ata aat gat ata tcc agt tgt ttg agt	528
Gln Met Ile Ser Leu Met Ala Ile Asn Asp Ile Ser Ser Cys Leu Ser	
165 170 175	
tat aat gca gct gtt ggt aaa aag ttt att gct ttg tcg att cct gtt	576
Tyr Asn Ala Ala Val Gly Lys Lys Phe Ile Ala Leu Ser Ile Pro Val	
180 185 190	
tta ctt cag ttt att att gca aac aac cca caa agc agc ata ttg caa	624
Leu Leu Gln Phe Ile Ile Ala Asn Asn Pro Gln Ser Ser Ile Leu Gln	
195 200 205	
aga ttg aaa tcg aat ctc cac gtt gaa gat gat ggg aag agg ttg tca	672
Arg Leu Lys Ser Asn Leu His Val Glu Asp Asp Gly Lys Arg Leu Ser	
210 215 220	
cgt gct cat ctg caa aaa tcc cat agc aaa att gcc caa caa att gat	720
Arg Ala His Leu Gln Lys Ser His Ser Lys Ile Ala Gln Gln Ile Asp	
225 230 235 240	
gat gat ttc acc aat gat tct tta acc ttg aca gat atc act gaa aag	768
Asp Asp Phe Thr Asn Asp Ser Leu Thr Leu Thr Asp Ile Thr Glu Lys	
245 250 255	
gca ttt tcg tcg atg aaa tct ttt ttc aat acc aat gct gcc agt caa	816
Ala Phe Ser Ser Met Lys Ser Phe Phe Asn Thr Asn Ala Ala Ser Gln	
260 265 270	
atc tct gaa gtg aca aga gct gtt gtc caa cac aat att ctc aat gga	864
Ile Ser Glu Val Thr Arg Ala Val Val Gln His Asn Ile Leu Asn Gly	
275 280 285	
acc gat ttg gag tgg gga gtc tca ttc ttg gaa tta tgt att act tgg	912
Thr Asp Leu Glu Trp Gly Val Ser Phe Leu Glu Leu Cys Ile Thr Trp	
290 295 300	
att cca gtt caa tta cgt ttt gtc agt ttg tcc acc ttg ttg gcc act	960
Ile Pro Val Gln Leu Arg Phe Val Ser Leu Ser Thr Leu Leu Ala Thr	
305 310 315 320	

tta ggt aga att aat att gaa ggt aac acc aaa tcc aat tac aac atg	1008
Leu Gly Arg Ile Asn Ile Glu Gly Asn Thr Lys Ser Asn Tyr Asn Met	
325 330 335	
caa ttc cag tat gct cgt tac ttg tta gga tta ctt tca tct cgt gtg	1056
Gln Phe Gln Tyr Ala Arg Tyr Leu Leu Gly Leu Leu Ser Ser Arg Val	
340 345 350	
aac atg att ggg tta tca gtt tca gat att att caa cag ttg tta tcg	1104
Asn Met Ile Gly Leu Ser Val Ser Asp Ile Ile Gln Gln Leu Leu Ser	
355 360 365	
ttg caa gct gat ttg att ttg aag gca agt gat ttg gac aaa agt gaa	1152
Leu Gln Ala Asp Leu Ile Leu Lys Ala Ser Asp Leu Asp Lys Ser Glu	
370 375 380	
att tca att tta aca gac att tat tct gac tgt att tgt agt ttg act	1200
Ile Ser Ile Leu Thr Asp Ile Tyr Ser Asp Cys Ile Cys Ser Leu Thr	
385 390 395 400	
aca cat ata tat tac ttt gat caa gtc ccg gac tcg att caa gaa atc	1248
Thr His Ile Tyr Tyr Phe Asp Gln Val Pro Asp Ser Ile Gln Glu Ile	
405 410 415	
tta atc aag att gat tac att tta gaa agc agt ttt gtg gaa gat aat	1296
Leu Ile Lys Ile Asp Tyr Ile Leu Glu Ser Ser Phe Val Glu Asp Asn	
420 425 430	
aac att acg tcc act gga gaa caa att caa gat ttg att atc caa ttg	1344
Asn Ile Thr Ser Thr Gly Glu Gln Ile Gln Asp Leu Ile Ile Gln Leu	
435 440 445	
ttg gat aac att tcg aag att ttt tta att ttg aag aat aaa tca agc	1392
Leu Asp Asn Ile Ser Lys Ile Phe Leu Ile Leu Lys Asn Lys Ser Ser	
450 455 460	
tca att aat cgt aac cat gtg aat ttg gaa cat tgg gat atc agt tta	1440
Ser Ile Asn Arg Asn His Val Asn Leu Glu His Trp Asp Ile Ser Leu	
465 470 475 480	
gga tta ttg gct cca caa ggc gac cat gat gat aac aga aaa atg att	1488
Gly Leu Leu Ala Pro Gln Gly Asp His Asp Asp Asn Arg Lys Met Ile	
485 490 495	
att tct acg aca caa ctt atc aat atc caa gcc agg tac ttg aaa gtg	1536
Ile Ser Thr Thr Gln Leu Ile Asn Ile Gln Ala Arg Tyr Leu Lys Val	
500 505 510	
ttt gat gag ttt ttg aat aat gaa ttg gcg gtt ggc aat tct aaa aag	1584
Phe Asp Glu Phe Leu Asn Asn Glu Leu Ala Val Gly Asn Ser Lys Lys	
515 520 525	
agc tat gat ctt ctt agc aaa cag tct cgt ttg gat cct gga agt aca	1632
Ser Tyr Asp Leu Leu Ser Lys Gln Ser Arg Leu Asp Pro Gly Ser Thr	
530 535 540	

gct gtt gaa gga gtg aac aag tct gac gat ctg gac aat ggt aag gac	1680
Ala Val Glu Gly Val Asn Lys Ser Asp Asp Leu Asp Asn Gly Lys Asp	
545 550 555 560	
ttt aaa aaa cct gat gcc aat caa tac att acc aat caa caa aac ttc	1728
Phe Lys Lys Pro Asp Ala Asn Gln Tyr Ile Thr Asn Gln Gln Asn Phe	
565 570 575	
ata tcc cat ttc ctt atg tat atc gac aaa ttt ttc gaa aat tac gat	1776
Ile Ser His Phe Leu Met Tyr Ile Asp Lys Phe Phe Glu Asn Tyr Asp	
580 585 590	
tcc ccc aac aca caa tca gtg tta ctt ttg gtt act gtt tta aaa gat	1824
Ser Pro Asn Thr Gln Ser Val Leu Leu Leu Val Thr Val Leu Lys Asp	
595 600 605	
atg atg aac att tta gga ttg aat ttc ttg agt aat ttt att cca ttt	1872
Met Met Asn Ile Leu Gly Leu Asn Phe Leu Ser Asn Phe Ile Pro Phe	
610 615 620	
ttc cac cat tgg gtt atg aaa gta aac aga gcc agt aat ttc act caa	1920
Phe His His Trp Val Met Lys Val Asn Arg Ala Ser Asn Phe Thr Gln	
625 630 635 640	
aga cag aaa ttc aaa gat act ttt gct cat att att tta tat tac atg	1968
Arg Gln Lys Phe Lys Asp Thr Phe Ala His Ile Ile Leu Tyr Tyr Met	
645 650 655	
ttg aaa gat ttg gat gag caa tat agt cat gat tta caa aat tat tgc	2016
Leu Lys Asp Leu Asp Glu Gln Tyr Ser His Asp Leu Gln Asn Tyr Cys	
660 665 670	
aaa agc tct aaa tta ttc aaa caa ata ttg gat gct gtt gaa tat aga	2064
Lys Ser Ser Lys Leu Phe Lys Gln Ile Leu Asp Ala Val Glu Tyr Arg	
675 680 685	
aaa atg caa aag ttt tgg gtc cat ggc att gac cct tca cca tct gat	2112
Lys Met Gln Lys Phe Trp Val His Gly Ile Asp Pro Ser Pro Ser Asp	
690 695 700	
ttg gaa aac act aaa ggc gac cgt acg ata ccc aca gat gcc aat ggt	2160
Leu Glu Asn Thr Lys Gly Asp Arg Thr Ile Pro Thr Asp Ala Asn Gly	
705 710 715 720	
aat tat att gct att aga atc aaa cct gaa aat att gag gaa ttt gcc	2208
Asn Tyr Ile Ala Ile Arg Ile Lys Pro Glu Asn Ile Glu Glu Phe Ala	
725 730 735	
tgt ggt aac aac ttt ttg att gta tgg tta cat ccc caa aaa caa tta	2256
Cys Gly Asn Asn Phe Leu Ile Val Trp Leu His Pro Gln Lys Gln Leu	
740 745 750	
ctc act gaa att gaa aaa tca caa gtc agt act cat atg agc aca ttc	2304
Leu Thr Glu Ile Glu Lys Ser Gln Val Ser Thr His Met Ser Thr Phe	
755 760 765	
aat aat gat tct aga aac aca aat atg aca gtg ata atg gat caa gga	2352

Asn	Asn	Asp	Ser	Arg	Asn	Thr	Asn	Met	Thr	Val	Ile	Met	Asp	Gln	Gly	
770						775					780					
tca	ctg	gca	cta	agt	gga	ggt	gca	gac	cat	gga	ggt	cac	ttt	ggt	ccg	2400
Ser	Leu	Ala	Leu	Ser	Gly	Gly	Ala	Asp	His	Gly	Gly	His	Phe	Val	Pro	
785					790					795					800	
cca	cct	gaa	ttt	ggt	aac	cac	acc	ggt	ttg	tct	tct	gaa	tct	gcg	tca	2448
Pro	Pro	Glu	Phe	Val	Asn	His	Thr	Gly	Leu	Ser	Ser	Glu	Ser	Ala	Ser	
				805					810					815		
tca	aac	tca	gag	aaa	ggt	ttg	tat	act	ggt	tta	gga	ttg	ggt	act	gct	2496
Ser	Asn	Ser	Glu	Lys	Gly	Leu	Tyr	Thr	Gly	Leu	Gly	Leu	Gly	Thr	Ala	
			820					825					830			
ggt	gat	att	act	atg	att	cat	tct	gaa	ata	tta	caa	tac	agt	caa	cat	2544
Gly	Asp	Ile	Thr	Met	Ile	His	Ser	Glu	Ile	Leu	Gln	Tyr	Ser	Gln	His	
		835					840					845				
ttc	caa	gaa	aga	ggt	tta	cct	cat	ggt	aat	ggg	ttt	gct	act	att	tta	2592
Phe	Gln	Glu	Arg	Gly	Leu	Pro	His	Gly	Asn	Gly	Phe	Ala	Thr	Ile	Leu	
	850					855					860					
cga	act	gtc	gat	agt	ggt	aac	agt	act	aat	gat	ggg	tta	att	tat	act	2640
Arg	Thr	Val	Asp	Ser	Val	Asn	Ser	Thr	Asn	Asp	Gly	Leu	Ile	Tyr	Thr	
865					870					875					880	
tat	gat	agt	aaa	tat	ttg	cag	tca	cca	aga	gta	agt	gat	ttg	aaa	gat	2688
Tyr	Asp	Ser	Lys	Tyr	Leu	Gln	Ser	Pro	Arg	Val	Ser	Asp	Leu	Lys	Asp	
				885					890					895		
gcc	atg	tca	aca	cat	agg	ggt	ata	agg	tta	tct	aaa	cca	aat	ttt	ggt	2736
Ala	Met	Ser	Thr	His	Arg	Gly	Ile	Arg	Leu	Ser	Lys	Pro	Asn	Phe	Gly	
			900					905					910			
ggt	gcc	aat	gga	act	gct	aat	atg	acg	gat	tct	gct	tct	aca	tcc	aat	2784
Gly	Ala	Asn	Gly	Thr	Ala	Asn	Met	Thr	Asp	Ser	Ala	Ser	Thr	Ser	Asn	
		915					920					925				
gga	tct	gtg	ttg	aat	aaa	aat	atg	caa	act	aca	gat	ggt	gat	tca	att	2832
Gly	Ser	Val	Leu	Asn	Lys	Asn	Met	Gln	Thr	Thr	Asp	Val	Asp	Ser	Ile	
		930					935				940					
tta	agt	ggt	ctt	gaa	agt	gaa	gac	gaa	gct	gcg	ttt	ggt	ggt	taa		2877
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<213> Candida albicans

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 20 25 30
 Tyr Leu Leu Tyr Tyr Ala Ser Thr Arg Arg Val Lys Leu Glu Lys Val
 35 40 45
 Ile Asn Phe Leu Lys Asp Lys Thr His His Asp Val Gly Arg Asn Arg
 50 55 60
 Thr Gly Asn Leu Gln Val Thr Leu Ala Ile Ile Gln Glu Leu Ile Lys
 65 70 75 80
 Lys Cys Ser Glu Asn Leu Asn Val Phe Ala Phe Gln Val Cys Tyr Ile
 85 90 95
 Leu Gln Leu Ile Ala Asn Thr Lys Asp Leu Ala Leu Cys Lys Asn Val
 100 105 110
 Val Lys Thr Phe Gly Val Leu Cys Glu Asn Leu Asp Gly Gly Leu Phe
 115 120 125
 Thr Gly Asp Lys Glu Phe Ile Lys Ile Phe Thr Glu Val Phe Gln Thr
 130 135 140
 Leu Val Ser Phe Gly Lys Asp Arg Ser Gly Val Thr Gln Tyr Asp Trp
 145 150 155 160
 Gln Met Ile Ser Leu Met Ala Ile Asn Asp Ile Ser Ser Cys Leu Ser
 165 170 175
 Tyr Asn Ala Ala Val Gly Lys Lys Phe Ile Ala Leu Ser Ile Pro Val
 180 185 190
 Leu Leu Gln Phe Ile Ile Ala Asn Asn Pro Gln Ser Ser Ile Leu Gln
 195 200 205
 Arg Leu Lys Ser Asn Leu His Val Glu Asp Asp Gly Lys Arg Leu Ser
 210 215 220
 Arg Ala His Leu Gln Lys Ser His Ser Lys Ile Ala Gln Gln Ile Asp
 225 230 235 240
 Asp Asp Phe Thr Asn Asp Ser Leu Thr Leu Thr Asp Ile Thr Glu Lys
 245 250 255
 Ala Phe Ser Ser Met Lys Ser Phe Phe Asn Thr Asn Ala Ala Ser Gln
 260 265 270
 Ile Ser Glu Val Thr Arg Ala Val Val Gln His Asn Ile Leu Asn Gly
 275 280 285
 Thr Asp Leu Glu Trp Gly Val Ser Phe Leu Glu Leu Cys Ile Thr Trp
 290 295 300
 Ile Pro Val Gln Leu Arg Phe Val Ser Leu Ser Thr Leu Leu Ala Thr
 305 310 315 320

Leu Gly Arg Ile Asn Ile Glu Gly Asn Thr Lys Ser Asn Tyr Asn Met
 325 330 335
 Gln Phe Gln Tyr Ala Arg Tyr Leu Leu Gly Leu Leu Ser Ser Arg Val
 340 345 350
 Asn Met Ile Gly Leu Ser Val Ser Asp Ile Ile Gln Gln Leu Leu Ser
 355 360 365
 Leu Gln Ala Asp Leu Ile Leu Lys Ala Ser Asp Leu Asp Lys Ser Glu
 370 375 380
 Ile Ser Ile Leu Thr Asp Ile Tyr Ser Asp Cys Ile Cys Ser Leu Thr
 385 390 395 400
 Thr His Ile Tyr Tyr Phe Asp Gln Val Pro Asp Ser Ile Gln Glu Ile
 405 410 415
 Leu Ile Lys Ile Asp Tyr Ile Leu Glu Ser Ser Phe Val Glu Asp Asn
 420 425 430
 Asn Ile Thr Ser Thr Gly Glu Gln Ile Gln Asp Leu Ile Ile Gln Leu
 435 440 445
 Leu Asp Asn Ile Ser Lys Ile Phe Leu Ile Leu Lys Asn Lys Ser Ser
 450 455 460
 Ser Ile Asn Arg Asn His Val Asn Leu Glu His Trp Asp Ile Ser Leu
 465 470 475 480
 Gly Leu Leu Ala Pro Gln Gly Asp His Asp Asp Asn Arg Lys Met Ile
 485 490 495
 Ile Ser Thr Thr Gln Leu Ile Asn Ile Gln Ala Arg Tyr Leu Lys Val
 500 505 510
 Phe Asp Glu Phe Leu Asn Asn Glu Leu Ala Val Gly Asn Ser Lys Lys
 515 520 525
 Ser Tyr Asp Leu Leu Ser Lys Gln Ser Arg Leu Asp Pro Gly Ser Thr
 530 535 540
 Ala Val Glu Gly Val Asn Lys Ser Asp Asp Leu Asp Asn Gly Lys Asp
 545 550 555 560
 Phe Lys Lys Pro Asp Ala Asn Gln Tyr Ile Thr Asn Gln Gln Asn Phe
 565 570 575
 Ile Ser His Phe Leu Met Tyr Ile Asp Lys Phe Phe Glu Asn Tyr Asp
 580 585 590
 Ser Pro Asn Thr Gln Ser Val Leu Leu Leu Val Thr Val Leu Lys Asp
 595 600 605
 Met Met Asn Ile Leu Gly Leu Asn Phe Leu Ser Asn Phe Ile Pro Phe
 610 615 620

Phe	His	His	Trp	Val	Met	Lys	Val	Asn	Arg	Ala	Ser	Asn	Phe	Thr	Gln	625	630	635	640
Arg	Gln	Lys	Phe	Lys	Asp	Thr	Phe	Ala	His	Ile	Ile	Leu	Tyr	Tyr	Met	645	650	655	
Leu	Lys	Asp	Leu	Asp	Glu	Gln	Tyr	Ser	His	Asp	Leu	Gln	Asn	Tyr	Cys	660	665	670	
Lys	Ser	Ser	Lys	Leu	Phe	Lys	Gln	Ile	Leu	Asp	Ala	Val	Glu	Tyr	Arg	675	680	685	
Lys	Met	Gln	Lys	Phe	Trp	Val	His	Gly	Ile	Asp	Pro	Ser	Pro	Ser	Asp	690	695	700	
Leu	Glu	Asn	Thr	Lys	Gly	Asp	Arg	Thr	Ile	Pro	Thr	Asp	Ala	Asn	Gly	705	710	715	720
Asn	Tyr	Ile	Ala	Ile	Arg	Ile	Lys	Pro	Glu	Asn	Ile	Glu	Glu	Phe	Ala	725	730	735	
Cys	Gly	Asn	Asn	Phe	Leu	Ile	Val	Trp	Leu	His	Pro	Gln	Lys	Gln	Leu	740	745	750	
Leu	Thr	Glu	Ile	Glu	Lys	Ser	Gln	Val	Ser	Thr	His	Met	Ser	Thr	Phe	755	760	765	
Asn	Asn	Asp	Ser	Arg	Asn	Thr	Asn	Met	Thr	Val	Ile	Met	Asp	Gln	Gly	770	775	780	
Ser	Leu	Ala	Leu	Ser	Gly	Gly	Ala	Asp	His	Gly	Gly	His	Phe	Val	Pro	785	790	795	800
Pro	Pro	Glu	Phe	Val	Asn	His	Thr	Gly	Leu	Ser	Ser	Glu	Ser	Ala	Ser	805	810	815	
Ser	Asn	Ser	Glu	Lys	Gly	Leu	Tyr	Thr	Gly	Leu	Gly	Leu	Gly	Thr	Ala	820	825	830	
Gly	Asp	Ile	Thr	Met	Ile	His	Ser	Glu	Ile	Leu	Gln	Tyr	Ser	Gln	His	835	840	845	
Phe	Gln	Glu	Arg	Gly	Leu	Pro	His	Gly	Asn	Gly	Phe	Ala	Thr	Ile	Leu	850	855	860	
Arg	Thr	Val	Asp	Ser	Val	Asn	Ser	Thr	Asn	Asp	Gly	Leu	Ile	Tyr	Thr	865	870	875	880
Tyr	Asp	Ser	Lys	Tyr	Leu	Gln	Ser	Pro	Arg	Val	Ser	Asp	Leu	Lys	Asp	885	890	895	
Ala	Met	Ser	Thr	His	Arg	Gly	Ile	Arg	Leu	Ser	Lys	Pro	Asn	Phe	Gly	900	905	910	
Gly	Ala	Asn	Gly	Thr	Ala	Asn	Met	Thr	Asp	Ser	Ala	Ser	Thr	Ser	Asn	915	920	925	

Gly Ser Val Leu Asn Asn Met Gln Thr Thr Asp Val Asp Ile
930 935 940

Leu Ser Gly Leu Glu Ser Glu Asp Glu Ala Ala Phe Val Val
945 950 955

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<213> Artificial Sequence

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Fragment to Sc YMR212c

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aaaggcaaaa acattcaagt tttcactaca ttttttgatt aattcctgaa taatggctaa 180
tgtgacttgt aaattaccag tacggtttct accaacatca tgatgagttt tatctttcaa 240
aaaattaatc accttttcta atttgactct acgagtggat gcatagtata ataaataact 300
taactcggac gagttgggtt ttttgtccac tgctttccca gcaggataac attgtaatat 360
taacttttga tgtttatggt gaaacaaatt cattcttgga tctggaagtt gaagaaacta 420
ttgaatcaaa acaggattta attaaccaat agaaaagaag taactcttga gttaaaaagg 480
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act ttg gat gaa ata aaa tat gcc atg aaa cat gtt ttc caa gat gct	96
Thr Leu Asp Glu Ile Lys Tyr Ala Met Lys His Val Phe Gln Asp Ala	
20 25 30	
caa tta ggt tta gca gga cat aga aaa tta gtg gta att ttg aaa aat	144
Gln Leu Gly Leu Ala Gly His Arg Lys Leu Val Val Ile Leu Lys Asn	
35 40 45	
gta ttt aaa aaa gcc att gaa tta aat caa att aat ttc ttt gcc atg	192
Val Phe Lys Lys Ala Ile Glu Leu Asn Gln Ile Asn Phe Phe Ala Met	
50 55 60	
tgt ttt act aaa ttg tta tct aaa gta tta cct ttg aaa aga gga gtt	240
Cys Phe Thr Lys Leu Ser Lys Val Leu Pro Leu Lys Arg Gly Val	
65 70 75 80	
ttg gca ggt gat aga ata gtc aaa ttt tgt tat ctg ttt gtt aat ggt	288
Leu Ala Gly Asp Arg Ile Val Lys Phe Cys Tyr Leu Phe Val Asn Gly	
85 90 95	
ctt gta aaa gat gcc aat gaa gaa aaa cgt tcc aaa gaa gaa gaa aaa	336
Leu Val Lys Asp Ala Asn Glu Glu Lys Arg Ser Lys Glu Glu Glu Lys	
100 105 110	
gaa gaa aaa gac aaa gac gaa gac aaa gat acg aat gaa agt gat aaa	384
Glu Glu Lys Asp Lys Asp Glu Asp Lys Asp Thr Asn Glu Ser Asp Lys	
115 120 125	
aat gaa gaa gat cag gaa gat caa gaa gga gaa gga gat caa gaa act	432
Asn Glu Glu Asp Gln Glu Asp Gln Glu Gly Glu Gly Asp Gln Glu Thr	
130 135 140	
cca att tcg gaa ttc ata tca tat ttg ata aaa tat tta ttg agt ggg	480
Pro Ile Ser Glu Phe Ile Ser Tyr Leu Ile Lys Tyr Leu Leu Ser Gly	
145 150 155 160	
ata gag gct aaa gat aaa ctg gtt cgt tat cgt gtt gta caa aca tta	528
Ile Glu Ala Lys Asp Lys Leu Val Arg Tyr Arg Val Val Gln Thr Leu	
165 170 175	
gca tac ttg gtt gaa ttc ttg acc gag ata cac gag aat aat aca ttg	576
Ala Tyr Leu Val Glu Phe Leu Thr Glu Ile His Glu Asn Asn Thr Leu	
180 185 190	
gaa gcg tta tat act tta tta agt aat agg cta caa gat aaa gag ctg	624
Glu Ala Leu Tyr Thr Leu Leu Ser Asn Arg Leu Gln Asp Lys Glu Leu	
195 200 205	
tcg ata cgt att caa gct gtt gtg gca tta tca cat ttt caa tta ttt	672
Ser Ile Arg Ile Gln Ala Val Val Ala Leu Ser His Phe Gln Leu Phe	
210 215 220	
gaa ttt agt att gaa ggt gat act gga gaa ttt gag gat gaa tta ata	720
Glu Phe Ser Ile Glu Gly Asp Thr Gly Glu Phe Glu Asp Glu Leu Ile	
225 230 235 240	
tca agt aac caa att cag aat aaa ttg ata aat tcc att caa aat gat	768

Ser Ser Asn Gln Ile Gln Asn Lys Leu Ile Asn Ser Ile Gln Asn Asp	245	250	255	
gat agt cca gaa gtc aga cgt gca gca tta atg aat ttg gtt aaa aca				816
Asp Ser Pro Glu Val Arg Arg Ala Ala Leu Met Asn Leu Val Lys Thr	260	265	270	
caa gat aca ata ccg att tta ctt gaa cga gcc aga gat tcc aat tct				864
Gln Asp Thr Ile Pro Ile Leu Leu Glu Arg Ala Arg Asp Ser Asn Ser	275	280	285	
att aat aga aga ttg gtt tat tct aaa ata gct cgt gaa tta ata act				912
Ile Asn Arg Arg Leu Val Tyr Ser Lys Ile Ala Arg Glu Leu Ile Thr	290	295	300	
gat ttg gat gat ctt gaa ttt gaa gat agg gaa ttt tta tta aaa tgg				960
Asp Leu Asp Asp Leu Glu Phe Glu Asp Arg Glu Phe Leu Leu Lys Trp	305	310	315	320
ggg tta aat gat cgt gat gaa act gtt aaa gca gcc gcc act aaa atg				1008
Gly Leu Asn Asp Arg Asp Glu Thr Val Lys Ala Ala Ala Thr Lys Met	325	330	335	
ctt acc att tat tgg tat caa tct gtc aat gaa gat tta tta gaa tta				1056
Leu Thr Ile Tyr Trp Tyr Gln Ser Val Asn Glu Asp Leu Leu Glu Leu	340	345	350	
att gat caa tta aat gtc aag agt gct ata gct gaa cag gcc ata tta				1104
Ile Asp Gln Leu Asn Val Lys Ser Ala Ile Ala Glu Gln Ala Ile Leu	355	360	365	
gca ttt ttt aaa aat aaa cca gaa gtt ctt gaa act att aaa att gat				1152
Ala Phe Phe Lys Asn Lys Pro Glu Val Leu Glu Thr Ile Lys Ile Asp	370	375	380	
gaa tca tat tgg aaa aat cta act aca gaa aag gca ttc ttg atg agg				1200
Glu Ser Tyr Trp Lys Asn Leu Thr Thr Glu Lys Ala Phe Leu Met Arg	385	390	395	400
acg ttt tat caa tat tgt aat gag aat caa tta cat gct tta atg gat				1248
Thr Phe Tyr Gln Tyr Cys Asn Glu Asn Gln Leu His Ala Leu Met Asp	405	410	415	
gcc aat ttc cct gaa tta ctt gat ttg tca ata aca tta gaa aag tat				1296
Ala Asn Phe Pro Glu Leu Leu Asp Leu Ser Ile Thr Leu Glu Lys Tyr	420	425	430	
ttg tca gtg agg ttg aaa act ata aat gaa aat gaa aat tta gtt aag				1344
Leu Ser Val Arg Leu Lys Thr Ile Asn Glu Asn Glu Asn Leu Val Lys	435	440	445	
aca tgg gaa act tat aat gcc aag att gac gaa tta gat gat caa ata				1392
Thr Trp Glu Thr Tyr Asn Ala Lys Ile Asp Glu Leu Asp Asp Gln Ile	450	455	460	
ttt agt ctt gaa aac cag att tcc aga ata aat act gat gcc gat aat				1440
Phe Ser Leu Glu Asn Gln Ile Ser Arg Ile Asn Thr Asp Ala Asp Asn				

465

470

475

480

ttc cgt aaa agt tta tct aac att gaa gaa gat att att gaa atc aat 1488
 Phe Arg Lys Ser Leu Ser Asn Ile Glu Glu Asp Ile Ile Glu Ile Asn
 485 490 495

att gct aag gat ttg ttc aaa aag aga att aaa caa ttg aaa aac aac 1536
 Ile Ala Lys Asp Leu Phe Lys Lys Arg Ile Lys Gln Leu Lys Asn Asn
 500 505 510

agt ggg aat cta gaa gat ttg att act gaa gaa aat caa gag att gct 1584
 Ser Gly Asn Leu Glu Asp Leu Ile Thr Glu Glu Asn Gln Glu Ile Ala
 515 520 525

gat caa atc aag gat ttc ctg atg gaa gat ttg caa caa caa ttg gaa 1632
 Asp Gln Ile Lys Asp Phe Leu Met Glu Asp Leu Gln Gln Gln Leu Glu
 530 535 540

gat atc aat aaa aat ctt gat gaa att gaa cat cat cca gaa gat ata 1680
 Asp Ile Asn Lys Asn Leu Asp Glu Ile Glu His His Pro Glu Asp Ile
 545 550 555 560

acg gct aaa tta gaa gaa ctt caa aca aaa tat gat tct tgt att agg 1728
 Thr Ala Lys Leu Glu Glu Leu Gln Thr Lys Tyr Asp Ser Cys Ile Arg
 565 570 575

gcg ctt gaa acc act agt gaa ttg aaa att cag act gtt caa atc ttt 1776
 Ala Leu Glu Thr Thr Ser Glu Leu Lys Ile Gln Thr Val Gln Ile Phe
 580 585 590

gaa caa gaa cat gaa aat gat tgt atc ccc ttt gta gat gct ttg aaa 1824
 Glu Gln Glu His Glu Asn Asp Cys Ile Pro Phe Val Asp Ala Leu Lys
 595 600 605

gaa tta gaa ttc att att aat caa tta tta tta att gtt aaa gat ttt 1872
 Glu Leu Glu Phe Ile Ile Asn Gln Leu Leu Leu Ile Val Lys Asp Phe
 610 615 620

gat tat gga gat gaa atg gca aga aga aaa ttg tta cat ata ata aga 1920
 Asp Tyr Gly Asp Glu Met Ala Arg Arg Lys Leu Leu His Ile Ile Arg
 625 630 635 640

atg aca tta act gaa gat aaa tta cct gat gcg tta ata tca gtg gca 1968
 Met Thr Leu Thr Glu Asp Lys Leu Pro Asp Ala Leu Ile Ser Val Ala
 645 650 655

ctt aga gta tta cga gca ctt tct ata aat gaa aaa gat ttt gtt tcc 2016
 Leu Arg Val Leu Arg Ala Leu Ser Ile Asn Glu Lys Asp Phe Val Ser
 660 665 670

atg gcg gta gaa ata att act gat att cgt gat tct cga gat gat gaa 2064
 Met Ala Val Glu Ile Ile Thr Asp Ile Arg Asp Ser Arg Asp Asp Glu
 675 680 685

gag ttc cat tct gct gcc gct aca ttt gat gat gat gat gat gat att 2112
 Glu Phe His Ser Ala Ala Ala Thr Phe Asp Asp Asp Asp Asp Ile
 690 695 700

ttg gga aat ggt gat gat gaa tct caa caa tca tca tca ctc agt gca	2160
Leu Gly Asn Gly Asp Asp Glu Ser Gln Gln Ser Ser Ser Leu Ser Ala	
705 710 715 720	
gta aca aag aag cga aga att gaa cca gat atg cca cca gat gat att	2208
Val Thr Lys Lys Arg Arg Ile Glu Pro Asp Met Pro Pro Asp Asp Ile	
725 730 735	
gtg tta aga tgt ctt acc atg aca caa tat gta ttg gaa gta att act	2256
Val Leu Arg Cys Leu Thr Met Thr Gln Tyr Val Leu Glu Val Ile Thr	
740 745 750	
cat agt ttg gat gat cat ctt tca ttg agt tct att tac agt ggt att	2304
His Ser Leu Asp Asp His Leu Ser Leu Ser Ser Ile Tyr Ser Gly Ile	
755 760 765	
gtc aat tat gct att cag aat gaa tcg aaa aag aaa tta tat ctt gct	2352
Val Asn Tyr Ala Ile Gln Asn Glu Ser Lys Lys Lys Leu Tyr Leu Ala	
770 775 780	
ggg tta act tgt tta gga ctt tat tct tta att gat tcc aaa att gcc	2400
Gly Leu Thr Cys Leu Gly Leu Tyr Ser Leu Ile Asp Ser Lys Ile Ala	
785 790 795 800	
aga att gca act aca aca tta tta ctg gca atg aga agt aat ggt gaa	2448
Arg Ile Ala Thr Thr Thr Leu Leu Leu Ala Met Arg Ser Asn Gly Glu	
805 810 815	
gaa gtg aaa gag att gga atg aaa gct att gtg gat ata ttg gca att	2496
Glu Val Lys Glu Ile Gly Met Lys Ala Ile Val Asp Ile Leu Ala Ile	
820 825 830	
tat ggt atg agt att ctt gat aaa tca tct aaa tac aaa tat tca aga	2544
Tyr Gly Met Ser Ile Leu Asp Lys Ser Ser Lys Tyr Lys Tyr Ser Arg	
835 840 845	
atg ttt ttc aaa gtt tta aat tca ttt gat gca cca aaa tta caa tgc	2592
Met Phe Phe Lys Val Leu Asn Ser Phe Asp Ala Pro Lys Leu Gln Cys	
850 855 860	
att gtc gct gaa gga tta tgc aaa ttg ttt tta gcc gat att ttg tac	2640
Ile Val Ala Glu Gly Leu Cys Lys Leu Phe Leu Ala Asp Ile Leu Tyr	
865 870 875 880	
aag act gac aaa cgg agt tta ttt gga aat gct att caa ggt ggt ggt	2688
Lys Thr Asp Lys Arg Ser Leu Phe Gly Asn Ala Ile Gln Gly Gly Gly	
885 890 895	
ggg ggt ggt ggt ggt aat gat gat cca act acc acc aat gac gat gaa	2736
Gly Gly Gly Gly Gly Asn Asp Asp Pro Thr Thr Thr Asn Asp Asp Glu	
900 905 910	
act gaa gaa gaa aca gat cga gag cat gaa aag cat tta ttt gaa gcg	2784
Thr Glu Glu Glu Thr Asp Arg Glu His Glu Lys His Leu Phe Glu Ala	
915 920 925	

att gta ctt att tat ttc aac ccc aac acc aaa tca aat caa gaa tta Ile Val Leu Ile Tyr Phe Asn Pro Asn Thr Lys Ser Asn Gln Glu Leu 930 935 940	2832
caa caa att ttg tca ttt tgt att cca gtt tat gcc ttt tct cat ata Gln Gln Ile Leu Ser Phe Cys Ile Pro Val Tyr Ala Phe Ser His Ile 945 950 955 960	2880
aat cat caa atc aat tta gct gca gtt agt ggt gat gtt att tat cga Asn His Gln Ile Asn Leu Ala Ala Val Ser Gly Asp Val Ile Tyr Arg 965 970 975	2928
ctt ttc act gaa aca gaa aca gaa tta tca cca agt gtt ata atc cct Leu Phe Thr Glu Thr Glu Thr Glu Leu Ser Pro Ser Val Ile Ile Pro 980 985 990	2976
caa tta ata tca tgg tgt gat cct cga aat tta gtt aaa tta tgc aat Gln Leu Ile Ser Trp Cys Asp Pro Arg Asn Leu Val Lys Leu Ser Asn 995 1000 1005	3024
gag gaa ata aat caa gca aca tca cat tta tgg caa tgt gtt tat tta Glu Glu Ile Asn Gln Ala Thr Ser His Leu Trp Gln Cys Val Tyr Leu 1010 1015 1020	3072
tta caa gtg gtt gaa caa gta gat gct cgt aat gtt aaa aga tgc atc Leu Gln Val Val Glu Gln Val Asp Ala Arg Asn Val Lys Arg Cys Ile 1025 1030 1035 1040	3120
att aac aat ttg aat aaa ttt cat ata acg gaa gaa tta gag tca aat Ile Asn Asn Leu Asn Lys Phe His Ile Thr Glu Glu Leu Glu Ser Asn 1045 1050 1055	3168
caa tta caa gct tta att aaa gct ctt gat gct aca gtt gaa tta ttt Gln Leu Gln Ala Leu Ile Lys Ala Leu Asp Ala Thr Val Glu Leu Phe 1060 1065 1070	3216
act aat aat gaa gat aac cct aat ttt atc ttg gat aaa cca aca aag Thr Asn Asn Glu Asp Asn Pro Asn Phe Ile Leu Asp Lys Pro Thr Lys 1075 1080 1085	3264
aag aat ttt gat act ttt att gaa tca ata aag aat aaa ttg gaa att Lys Asn Phe Asp Thr Phe Ile Glu Ser Ile Lys Asn Lys Leu Glu Ile 1090 1095 1100	3312
gct caa aaa aga gaa gaa aat gaa ctg att aaa agt ggt aca aat tca Ala Gln Lys Arg Glu Glu Asn Glu Leu Ile Lys Ser Gly Thr Asn Ser 1105 1110 1115 1120	3360
ata tta cat gaa tta gat gat tta gat att gga act gga gag agt agt Ile Leu His Glu Leu Asp Asp Leu Asp Ile Gly Thr Gly Glu Ser Ser 1125 1130 1135	3408
caa ata tct ata aaa tca gaa aca aaa aga aga gat ctg gat cga tct Gln Ile Ser Ile Lys Ser Glu Thr Lys Arg Arg Asp Leu Asp Arg Ser 1140 1145 1150	3456
ctg caa gtt agt aaa act acg tca cca gaa act tca gaa aat gaa gat	3504

Leu Gln Val Ser Lys	Thr Ser Pro Glu Thr Ser Glu Asn Glu Asp	
1155	1160	1165
gaa gag gat gat aat gag gag gag gaa caa gag aag aag aaa agt ttt		3552
Glu Glu Asp Asp Asn Glu Glu Glu Glu Gln Glu Lys Lys Lys Ser Phe		
1170	1175	1180
act gat gga aaa aat aaa ctt gaa cta aag gca gat aag cca atc aca		3600
Thr Asp Gly Lys Asn Lys Leu Glu Leu Lys Ala Asp Lys Pro Ile Thr		
1185	1190	1200
ttt aaa gct gaa gac aag agg gaa ggg tca gtt gaa aca gat cat ggt		3648
Phe Lys Ala Glu Asp Lys Arg Glu Gly Ser Val Glu Thr Asp His Gly		
1205	1210	1215
caa gaa caa gtt cta gtt gaa tca aag aaa gtc att gat agt aat gtt		3696
Gln Glu Gln Val Leu Val Glu Ser Lys Lys Val Ile Asp Ser Asn Val		
1220	1225	1230
gaa gat tct tta gaa gat ata gat aag ttt tta gaa gaa gca gat gat		3744
Glu Asp Ser Leu Glu Asp Ile Asp Lys Phe Leu Glu Glu Ala Asp Asp		
1235	1240	1245
gtt gat tat ggt gat att tca atg gat		3771
Val Asp Tyr Gly Asp Ile Ser Met Asp		
1250	1255	

<210> 21
 <211> 1257
 <212> PRT
 <213> Candida albicans

<400> 21

Met Asp Ile Pro Pro Lys Pro Thr Leu Lys Ala Ile Lys Lys Phe Arg	
1 5 10 15	
Thr Leu Asp Glu Ile Lys Tyr Ala Met Lys His Val Phe Gln Asp Ala	
20 25 30	
Gln Leu Gly Leu Ala Gly His Arg Lys Leu Val Val Ile Leu Lys Asn	
35 40 45	
Val Phe Lys Lys Ala Ile Glu Leu Asn Gln Ile Asn Phe Phe Ala Met	
50 55 60	
Cys Phe Thr Lys Leu Leu Ser Lys Val Leu Pro Leu Lys Arg Gly Val	
65 70 75 80	
Leu Ala Gly Asp Arg Ile Val Lys Phe Cys Tyr Leu Phe Val Asn Gly	
85 90 95	
Leu Val Lys Asp Ala Asn Glu Glu Lys Arg Ser Lys Glu Glu Glu Lys	
100 105 110	
Glu Glu Lys Asp Lys Asp Glu Asp Lys Asp Thr Asn Glu Ser Asp Lys	
115 120 125	

Asn	Glu	Glu	Asp	Gln	Glu	Asp	Gln	Glu	Gly	Glu	Gly	Asp	Gln	Glu	Thr	130	135	140
Pro	Ile	Ser	Glu	Phe	Ile	Ser	Tyr	Leu	Ile	Lys	Tyr	Leu	Leu	Ser	Gly	145	150	155
Ile	Glu	Ala	Lys	Asp	Lys	Leu	Val	Arg	Tyr	Arg	Val	Val	Gln	Thr	Leu	165	170	175
Ala	Tyr	Leu	Val	Glu	Phe	Leu	Thr	Glu	Ile	His	Glu	Asn	Asn	Thr	Leu	180	185	190
Glu	Ala	Leu	Tyr	Thr	Leu	Leu	Ser	Asn	Arg	Leu	Gln	Asp	Lys	Glu	Leu	195	200	205
Ser	Ile	Arg	Ile	Gln	Ala	Val	Val	Ala	Leu	Ser	His	Phe	Gln	Leu	Phe	210	215	220
Glu	Phe	Ser	Ile	Glu	Gly	Asp	Thr	Gly	Glu	Phe	Glu	Asp	Glu	Leu	Ile	225	230	235
Ser	Ser	Asn	Gln	Ile	Gln	Asn	Lys	Leu	Ile	Asn	Ser	Ile	Gln	Asn	Asp	245	250	255
Asp	Ser	Pro	Glu	Val	Arg	Arg	Ala	Ala	Leu	Met	Asn	Leu	Val	Lys	Thr	260	265	270
Gln	Asp	Thr	Ile	Pro	Ile	Leu	Leu	Glu	Arg	Ala	Arg	Asp	Ser	Asn	Ser	275	280	285
Ile	Asn	Arg	Arg	Leu	Val	Tyr	Ser	Lys	Ile	Ala	Arg	Glu	Leu	Ile	Thr	290	295	300
Asp	Leu	Asp	Asp	Leu	Glu	Phe	Glu	Asp	Arg	Glu	Phe	Leu	Leu	Lys	Trp	305	310	315
Gly	Leu	Asn	Asp	Arg	Asp	Glu	Thr	Val	Lys	Ala	Ala	Ala	Thr	Lys	Met	325	330	335
Leu	Thr	Ile	Tyr	Trp	Tyr	Gln	Ser	Val	Asn	Glu	Asp	Leu	Leu	Glu	Leu	340	345	350
Ile	Asp	Gln	Leu	Asn	Val	Lys	Ser	Ala	Ile	Ala	Glu	Gln	Ala	Ile	Leu	355	360	365
Ala	Phe	Phe	Lys	Asn	Lys	Pro	Glu	Val	Leu	Glu	Thr	Ile	Lys	Ile	Asp	370	375	380
Glu	Ser	Tyr	Trp	Lys	Asn	Leu	Thr	Thr	Glu	Lys	Ala	Phe	Leu	Met	Arg	385	390	395
Thr	Phe	Tyr	Gln	Tyr	Cys	Asn	Glu	Asn	Gln	Leu	His	Ala	Leu	Met	Asp	405	410	415
Ala	Asn	Phe	Pro	Glu	Leu	Leu	Asp	Leu	Ser	Ile	Thr	Leu	Glu	Lys	Tyr	420	425	430

Leu Ser Val Arg Leu Lys Thr Ile Asn Glu Asn Glu Asn Leu Val Lys
 435 440 445
 Thr Trp Glu Thr Tyr Asn Ala Lys Ile Asp Glu Leu Asp Asp Gln Ile
 450 455 460
 Phe Ser Leu Glu Asn Gln Ile Ser Arg Ile Asn Thr Asp Ala Asp Asn
 465 470 475 480
 Phe Arg Lys Ser Leu Ser Asn Ile Glu Glu Asp Ile Ile Glu Ile Asn
 485 490 495
 Ile Ala Lys Asp Leu Phe Lys Lys Arg Ile Lys Gln Leu Lys Asn Asn
 500 505 510 -
 Ser Gly Asn Leu Glu Asp Leu Ile Thr Glu Glu Asn Gln Glu Ile Ala
 515 520 525
 Asp Gln Ile Lys Asp Phe Leu Met Glu Asp Leu Gln Gln Gln Leu Glu
 530 535 540
 Asp Ile Asn Lys Asn Leu Asp Glu Ile Glu His His Pro Glu Asp Ile
 545 550 555 560
 Thr Ala Lys Leu Glu Glu Leu Gln Thr Lys Tyr Asp Ser Cys Ile Arg
 565 570 575
 Ala Leu Glu Thr Thr Ser Glu Leu Lys Ile Gln Thr Val Gln Ile Phe
 580 585 590
 Glu Gln Glu His Glu Asn Asp Cys Ile Pro Phe Val Asp Ala Leu Lys
 595 600 605
 Glu Leu Glu Phe Ile Ile Asn Gln Leu Leu Leu Ile Val Lys Asp Phe
 610 615 620
 Asp Tyr Gly Asp Glu Met Ala Arg Arg Lys Leu Leu His Ile Ile Arg
 625 630 635 640
 Met Thr Leu Thr Glu Asp Lys Leu Pro Asp Ala Leu Ile Ser Val Ala
 645 650 655
 Leu Arg Val Leu Arg Ala Leu Ser Ile Asn Glu Lys Asp Phe Val Ser
 660 665 670
 Met Ala Val Glu Ile Ile Thr Asp Ile Arg Asp Ser Arg Asp Asp Glu
 675 680 685
 Glu Phe His Ser Ala Ala Ala Thr Phe Asp Asp Asp Asp Asp Ile
 690 695 700
 Leu Gly Asn Gly Asp Asp Glu Ser Gln Gln Ser Ser Ser Leu Ser Ala
 705 710 715 720
 Val Thr Lys Lys Arg Arg Ile Glu Pro Asp Met Pro Pro Asp Asp Ile
 725 730 735

Val	Leu	Arg	Cys	Leu	Thr	Met	Thr	Gln	Tyr	Val	Leu	Glu	Val	Ile	Thr	740	745	750
His	Ser	Leu	Asp	Asp	His	Leu	Ser	Leu	Ser	Ser	Ile	Tyr	Ser	Gly	Ile	755	760	765
Val	Asn	Tyr	Ala	Ile	Gln	Asn	Glu	Ser	Lys	Lys	Lys	Leu	Tyr	Leu	Ala	770	775	780
Gly	Leu	Thr	Cys	Leu	Gly	Leu	Tyr	Ser	Leu	Ile	Asp	Ser	Lys	Ile	Ala	785	790	795
Arg	Ile	Ala	Thr	Thr	Thr	Leu	Leu	Leu	Ala	Met	Arg	Ser	Asn	Gly	Glu	805	810	815
Glu	Val	Lys	Glu	Ile	Gly	Met	Lys	Ala	Ile	Val	Asp	Ile	Leu	Ala	Ile	820	825	830
Tyr	Gly	Met	Ser	Ile	Leu	Asp	Lys	Ser	Ser	Lys	Tyr	Lys	Tyr	Ser	Arg	835	840	845
Met	Phe	Phe	Lys	Val	Leu	Asn	Ser	Phe	Asp	Ala	Pro	Lys	Leu	Gln	Cys	850	855	860
Ile	Val	Ala	Glu	Gly	Leu	Cys	Lys	Leu	Phe	Leu	Ala	Asp	Ile	Leu	Tyr	865	870	875
Lys	Thr	Asp	Lys	Arg	Ser	Leu	Phe	Gly	Asn	Ala	Ile	Gln	Gly	Gly	Gly	885	890	895
Gly	Gly	Gly	Gly	Gly	Asn	Asp	Asp	Pro	Thr	Thr	Thr	Asn	Asp	Asp	Glu	900	905	910
Thr	Glu	Glu	Glu	Thr	Asp	Arg	Glu	His	Glu	Lys	His	Leu	Phe	Glu	Ala	915	920	925
Ile	Val	Leu	Ile	Tyr	Phe	Asn	Pro	Asn	Thr	Lys	Ser	Asn	Gln	Glu	Leu	930	935	940
Gln	Gln	Ile	Leu	Ser	Phe	Cys	Ile	Pro	Val	Tyr	Ala	Phe	Ser	His	Ile	945	950	955
Asn	His	Gln	Ile	Asn	Leu	Ala	Ala	Val	Ser	Gly	Asp	Val	Ile	Tyr	Arg	965	970	975
Leu	Phe	Thr	Glu	Thr	Glu	Thr	Glu	Leu	Ser	Pro	Ser	Val	Ile	Ile	Pro	980	985	990
Gln	Leu	Ile	Ser	Trp	Cys	Asp	Pro	Arg	Asn	Leu	Val	Lys	Leu	Ser	Asn	995	1000	1005
Glu	Glu	Ile	Asn	Gln	Ala	Thr	Ser	His	Leu	Trp	Gln	Cys	Val	Tyr	Leu	1010	1015	1020
Leu	Gln	Val	Val	Glu	Gln	Val	Asp	Ala	Arg	Asn	Val	Lys	Arg	Cys	Ile	1025	1030	1035

Ile Asn Asn Leu Asn Lys Phe His Ile Thr Glu Glu Leu Glu Ser Asn
1045 1050 1055

Gln Leu Gln Ala Leu Ile Lys Ala Leu Asp Ala Thr Val Glu Leu Phe
1060 1065 1070

Thr Asn Asn Glu Asp Asn Pro Asn Phe Ile Leu Asp Lys Pro Thr Lys
1075 1080 1085

Lys Asn Phe Asp Thr Phe Ile Glu Ser Ile Lys Asn Lys Leu Glu Ile
1090 1095 1100

Ala Gln Lys Arg Glu Glu Asn Glu Leu Ile Lys Ser Gly Thr Asn Ser
1105 1110 1115 1120

Ile Leu His Glu Leu Asp Asp Leu Asp Ile Gly Thr Gly Glu Ser Ser
1125 1130 1135

Gln Ile Ser Ile Lys Ser Glu Thr Lys Arg Arg Asp Leu Asp Arg Ser
1140 1145 1150

Leu Gln Val Ser Lys Thr Thr Ser Pro Glu Thr Ser Glu Asn Glu Asp
1155 1160 1165

Glu Glu Asp Asp Asn Glu Glu Glu Glu Gln Glu Lys Lys Lys Ser Phe
1170 1175 1180

Thr Asp Gly Lys Asn Lys Leu Glu Leu Lys Ala Asp Lys Pro Ile Thr
1185 1190 1195 1200

Phe Lys Ala Glu Asp Lys Arg Glu Gly Ser Val Glu Thr Asp His Gly
1205 1210 1215

Gln Glu Gln Val Leu Val Glu Ser Lys Lys Val Ile Asp Ser Asn Val
1220 1225 1230

Glu Asp Ser Leu Glu Asp Ile Asp Lys Phe Leu Glu Glu Ala Asp Asp
1235 1240 1245

Val Asp Tyr Gly Asp Ile Ser Met Asp
1250 1255

<210> 22

<211> 603

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Homologous
Fragment to Sc YDR325

<400> 22

ctgtttgtta atggtcttgt aaaagatgcc aatgaagaaa aacgttccaa agaagaagaa 60

aaagaagaga aagacaaaga caaagacaaa gatacgaatg aaagtgataa aaatgaagaa 120

gatcaggaag atcaagaagg agaaggagat caagaaactc caatttcgga attcatatca 180
tatttgataa aatatttatt gagtgggata gaggctaaag ataaactggg tcgttatcgt 240
gttggtacaaa cattagcata cttgggttgaa ttcttgaccg agatacacga gaataataca 300
ttggaagcgt tatatacttt attaagtaat aggctacaag ataaagagct gtcgatacgt 360
attcaagctg ttgtggcatt atcacatttt caattatttg aatttagtat tgaagggtgat 420
actggagaat ttgaggatga attaatatca agtaaccaa ttcagaataa attgataaat 480
tccattcaaa atgatgatag tccagaagtc agacgtgcag cattaatgaa tttgggttaa 540
acacaagata caataccgat tttacttgag cgagccagag attccaattc tattaataga 600
aga 603

<210> 23
<211> 581
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Homologous
Fragment to Sc YDR325

<400> 23
gggggttaaat gatcgtgatg aatctgttaa agcagccgcc tttaaaatgc taaccattta 60
ttggtatcaa tctgtcaatg aagatttatt agaattaatt gatcaattaa atgtcagaag 120
tgctatagct gaacaggcca tattagcatt ttttaaaaat aaaccagaag ttcttgcaac 180
tattaaaatt gatgaatcat attggaaaaa tctaactaca gaaaaggcat tcttgatgag 240
gacgttttat caatattgta atgagaatca attacatgct ttaatggatg ccaatttccc 300
tgaattactt gatttgtcaa taacattaga aaagtatttg tcagtgaggt tgaaaacaat 360
aaatgaaaat gaaaatttaa ttaagacatg ggaaacttat aatgccaaga ttgacgaatt 420
agatgatcaa atatttagtc ttgaaaacca gatttccaga ataaatactg atgccgataa 480
tttccgtaaa agtttatcta acattgaaga agatattatt gaaatcaata ttgctaagga 540
tttggtcaaa aagagaatta aaqaattgaa aaactgagca c 581

<210> 24
<211> 662
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Homologous
Fragment to Sc YDR325

<400> 24

tggtgactca attcatttga tgcacaaaaa ttacaatgca ttgtcgctga gtagattatg 60
caaattgttt ttagccgata ttttgtacaa gactgacaaa cggatttatt tggaaatgct 120
attcaaggtg gtggtggtgg tgatgatcca actaccacca atgacgatga aactgaagaa 180
gaaacagatc gagagcatga aaagcattta tttgaagcga ttgtacttat ttatttcaac 240
cccaacacca aatcaaatac agaattacaa caaattttgt cattttgtat tccagtttat 300
gccttttctc atataaatca tcaaatacat ttagctgcag ttagtggtga tgttatttat 360
cgacttttca ctgaaacaga aacagaatta tcaccaagtg ttataatccc tcaattaata 420
tcatggtgtg atcctcgaaa tttagttaaa ttatcgaatg aggaaataaa tcaagcaaca 480
tcacatttat ggcaatgtgt ttatttatta caagtgggtg aacaagtaga tgctcgtaat 540
gttaaaagat gcatcattaa caatttgaat aaatttcata taacggaaga attagaatca 600
aatcaattac aagctttaat taaagctctt gatgctacag ttgaattatt tactaataat 660
ga 662

<210> 25

<211> 231

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Homologous
Fragment to Sc YOR110

<400> 25

atatgtgttg atagttacac atgcagcaac gaaaattgct ttaggatcag ctttattaca 60
gttaaaatca gttactgatg ttatagatga taatcaaact gtgttacgtg ctggtgcatg 120
ttcattatcc aaatttggtg gagatggcga agataaaacc aatcatacta ttcaatggaa 180
aattgtcatg aatggtaatt gtgaattctt gacacagggt gaagaaatga a 231